

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 16:18:06 ; Search time 282 Seconds
(without alignments)
134.842 Million cell updates/sec

Title: US-09-830-691a-3

Perfect score: 573

Sequence: 1 MNVPKTRRYCKGKCKKH.....RCKHFELGGDKTKGAISF 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_238sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	100.0	106	3	AAY94261 Phaffia r
2	495	86.4	106	2	AAR77658 Ribosomal
3	490	85.5	105	7	ADC88814 Ribosomal
4	490	85.5	106	3	AAY55842 P. ciferr
5	483	84.3	106	2	AAW57490 Amino aci
6	483	84.3	106	7	ADC88117 Ribosomal
7	482	84.1	106	4	AAG70870 C albican
8	481	83.9	106	4	AAG70742 S cerevis
9	478	83.4	102	7	ADC88813 Ribosomal
10	478	83.4	116	4	AAG70795 S cerevis
11	476	83.1	105	7	ADC88816 Ribosomal
12	471	82.2	105	7	ADC88805 Ribosomal
13	463	80.8	105	7	ADC88810 Ribosomal
14	462	80.6	106	2	AAR32293 Sequence
15	461	80.5	105	7	ADC88118 Ribosomal
16	460	80.3	105	7	ADC88803 Ribosomal
17	460	80.3	105	7	ADC88024 Ribosomal
18	459	80.1	105	3	AAG22309 Zea mays
19	459	80.1	105	3	AAG19042 Zea mays
20	458	79.9	105	3	AAG33740 Arabidops
21	458	79.9	105	3	AAG37808 Arabidops
22	458	79.9	105	3	AAG10245 Arabidops
23	458	79.9	105	3	AAG45312 Arabidops
24	458	79.9	105	7	ADC88800 Ribosomal
25	458	79.9	105	7	ADE25075 Plant gro

26	458	79.9	122	3	AAG33739 Arabidops
27	457	79.8	105	7	ADC88809 Ribosomal
28	452	78.9	104	7	ADC88806 Ribosomal
29	450	78.5	106	8	ADO57261 Kidney de
30	439.5	76.7	104	7	ADC88802 Ribosomal
31	439	76.6	106	7	ADE59095 Human Pro
32	439	76.6	131	3	AAB43900 Human can
33	436	76.1	106	5	ABP65233 Hypoxia-r
34	436	76.1	137	5	ABP41758 Human ova
35	434	75.7	105	7	ADC88808 Ribosomal
36	434	75.7	105	7	ADE59093 Rat Prote
37	434	75.7	105	7	ADE62528 Human Pro
38	434	75.7	111	5	ABP42647 Human Pro
39	431.5	75.3	105	7	ADC88801 Ribosomal
40	428	74.7	106	5	ABG32266 Human rib
41	428	74.7	106	5	ABG32265 Human rib
42	424	74.0	127	5	ABP64899 Human pro
43	424	74.0	147	4	ABG27187 Novel hum
44	422	73.6	138	4	ABG16314 Novel hum
45	404	70.5	122	4	ABB63267 Drosophill

ALIGNMENTS

RESULT 1
AAY94261
ID AAY94261 standard; protein; 106 AA.
XX
AC AAY94261;
XX
DT 12-SEP-2003 (revised)
DT 25-SEP-2000 (first entry)
XX
DE Phaffia rhodozyma L41.
XX
KW Astaxanthin; L41; Yeast; carotenoid; cyclohexamide-resistance;
KW site-directed mutagenesis; selectable marker; ribosomal protein.
XX
OS Xanthophyllomyces dendrorhous.
XX
PN WO200026387-A1.
XX
PD 11-MAY-2000.
XX
PF 29-MAY-1999; 99WO-KR000265.
XX
PR 31-OCT-1998; 98KR-00046547.
XX
(KOAD) KOREA ADV INST SCI & TECHNOLOGY.
(HAIT-) HAI TAI CONFECTIONERY CO LTD.

Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;
Choi SK, Son YR;

WPI; 2000-365630/31.

N-PSDB; AAA15567, AAA15568.

Novel vector comprising a cyclohexamide-resistance gene and a ribosomal DNA useful for the transformation of Phaffia rhodozyma.

Claim 1; Page 37-38; 43pp; English.

The present sequence is the Phaffia rhodozyma L41 ribosomal protein. The mutated form of the L41 protein, with a glutamine at position 56, instead of a proline (as there is in the wild-type protein) confers cycloheximide resistance on the cell carrying the mutated form of the gene. The mutated form can be produced by site-directed mutagenesis. This antibiotic resistance phenotype can be exploited by using this gene as a selectable marker in a P. rhodozyma vector. The vector can be used to carry foreign DNA, e.g. the astaxanthin gene, a carotenoid. (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 106 AA;
 Query Match 100.0%; Score 573; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 7.2e-61;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNVPTRRYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60
 DB 1 MNNVPTRRYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

QY 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106
 DB 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106

RESULT 2
 AAR77658
 ID AAR77658 standard; protein; 106 AA.
 XX
 AC AAR77658;
 XX
 DT 16-OCT-2003 (revised)
 DT 03-DEC-1996 (first entry)
 XX
 DE Ribosomal protein L41.
 XX
 KW Ribosomal protein; expression vector; heterogene; yeast; GAP; PGK; PMA;
 KW phosphoglyceric acid kinase; protoplasmic membrane proton ATPase;
 KW glyceraldehyde-3-phosphoric acid dehydrogenase; resistance marker;
 KW hygromycin B phosphotransferase; aminoglycoside-3'-phosphotransferase.
 XX
 OS Pichia jadinii.
 XX
 FN WO9532289-A1.
 XX
 PD 30-NOV-1995.
 XX
 PF 25-MAY-1995; 95WO-JP001005.
 XX
 PR 25-MAY-1994; 94JP-00135015.
 PR 26-OCT-1994; 94JP-00285823.
 PR 28-APR-1995; 95JP-00129287.
 XX
 PA (KIRI) KIRIN BEER KK.
 XX
 XX Kondo K, Kajiwara S, Misawa N;
 PI N-PSDB; AAT08602.
 DR WPI; 1996-020584/02.
 DR N-PSDB; AAT08602.
 PT Ribosomal protein L41 gene, promoter and terminator sequences, isolated
 PT from Candida utilis - used in vector for expression of hetero:gene(s) in
 PT yeast.
 XX
 PS Claim 2; Page 162; 252pp; Japanese.
 XX
 CC The L41 ribosomal structural protein gene can be used in the construction
 CC of expression vectors designed specifically to express heterogenes in
 CC yeast. The vectors also comprise: a promoter and terminator sequence
 CC selected from phosphoglyceric acid kinase (PGK), glyceraldehyde-3-
 CC phosphoric acid dehydrogenase (GAP) and protoplasmic membrane proton
 CC ATPase (PMA) genes isolated from Candida utilis; a drug resistance marker
 CC selected from aminoglycoside-3'-phosphotransferase or hygromycin B
 CC phosphotransferase; and the heterogene to be expressed. L41 confers
 CC cyclohexamine resistance on the yeast. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 106 AA;
 Query Match 86.4%; Score 495; DB 2; Length 106;
 Best Local Similarity 85.8%; Pred. No. 1.8e-51;
 Matches 91; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNNVPTRRYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60
 DB 1 MNNVPTRRYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

QY 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106
 DB 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106

RESULT 3
 ADC88814
 ID ADC88814 standard; protein; 105 AA.
 XX
 AC ADC88814;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Ribosomal protein similar to FCWP1 #1030.
 XX
 KW Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
 KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
 KW Colletotrichum; Diplodia; Fusarium; Gaumanomyces; Helminthosporium;
 KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
 KW Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
 KW Septoria; Thielaviopsis; Venturia; Verticillium.
 XX
 OS Unidentified.
 XX
 FN US6573361-B1.
 XX
 PD 03-JUN-2003.
 XX
 PF 07-DEC-2000; 2000US-00732210.
 XX
 PR 07-DEC-1999; 99US-0169340P.
 PR 07-DEC-1999; 99US-0169513P.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
 PI WPI; 2003-754558/71.
 DR
 PT Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
 PT for controlling fungal infections in plants.
 XX
 PS Example 21; SEQ ID NO 1067; 27pp; English.
 XX
 CC The invention relates to an isolated antifungal ribosomal protein from
 CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein AlyAPP from Alyssum and FCWP1,
 CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by Alternaria (e.g. Alternaria brassicola, Alternaria solani),
 CC Ascochyta (e.g. Ascochyta pisi), Botrytis (e.g. Botrytis cinerea),
 CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
 CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
 CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
 CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
 CC moniliforme, Fusarium roseum), Gaumanomyces (e.g. Gaumanomyces
 CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
 CC graminis f.sp. tritici), Helminthosporium maydis), Macrophomina
 CC (e.g. Macrophomina phaseolina, Maganaporthe grisea), Mycosphaerella
 CC (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca), Phoma
 CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
 CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
 CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
 CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
 CC citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora
 CC infestans), Plasmopara (e.g. Plasmopara viticola), Podosphaera (e.g.
 CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia
 CC striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,

CC Puccinia recondita, Puccinia atachidis, Puthium (e.g. Puthium
 CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
 CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
 CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
 CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
 CC Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora
 CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
 CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
 CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
 CC Verticillium albo-atrum). Mutations in the proteolytic consensus
 CC sequences contained within FCWP1 provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWP1. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX
 SQ Sequence 105 AA;

Query Match 85.5%; Score 490; DB 7; Length 105;
 Best Local Similarity 85.7%; Pred. No. 7.2e-51;
 Matches 90; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 Qy 2 VNVPTRTTYCKGKCKKHTPHKVTQYKKGDSIFAQGRYDRKQSGYGQTKPVFHK 61
 Db 1 VNVPTRTTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKQSGYGQTKPVFHK 60
 Qy 62 AKTTKKVLRLECSVCCKYKQMTLKRCKHFGELGDKTKGAATSF 106
 Db 61 AKTTKKVLRLECVCKTKAQLAKRCKHFGELGDKTKGQALQF 105

RESULT 4
 AAY55842
 ID AAY55842 standard; protein; 106 AA.

XX AC AAY55842;
 XX DT 06-MAR-2000 (first entry)
 XX DE P. ciferrii ribosomal protein.
 XX KW L41 gene; ribosomal protein; CYHR gene; cyclohexamide resistance;
 XX KW tetraacetyl phytosphingosine; TAPS; ceramide; skin-protection;
 XX KW water-loss; skin drying; cosmetic.
 XX OS Pichia ciferrii.
 XX PN WO9957279-A1.
 XX PD 11-NOV-1999.
 XX PF 31-OCT-1998; 98WO-KR000346.
 XX PR 07-MAY-1998; 98KR-00016309.
 XX PR 07-MAY-1998; 98KR-00016310.
 XX PR 21-AUG-1998; 98KR-00033969.
 XX (DOOS-) DOOSAN CORP.
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 XX Rhee SK, Bae JH, Choi ES, Sohn JH, Kang HA, Park CS;
 XX WPI; 2000-062149/05.
 DR N-PSDB; AAZ39763.
 XX New expression cassettes comprising CYHR gene resistant to cyclohexamide
 PT and desired gene, used for transforming Pichia ciferrii to produce
 PT tetraacetyl phytosphingosine.
 XX Example 3; Page 50-52; 72pp; English.

XX The invention provides an expression cassette for a desired gene in P.
 CC ciferrii that comprises: (a) a P. ciferrii ribosomal DNA operably linked
 CC to; (b) a CYHR gene (L41 gene in which Pro56 is replaced with Glu to give
 CC cyclohexamide resistance) which is responsible for cyclohexamide,
 CC operably linked to; and (c) a desired structural gene. The ribosomal L41-
 CC coding gene was manipulated to give resistance to cyclohexamide, so it
 CC can be used as a selection marker. The expression cassette is used to
 CC transform P. ciferrii, especially to produce higher levels of tetraacetyl
 CC phytosphingosine (TAPS) in a shorter space of time. TAPS is a precursor
 CC of ceramides, and shows skin-protection activity, and prevents excessive
 CC water-loss and drying out of the skin, and so is of great use in
 CC cosmetics. The method is used for producing P. ciferrii mutants which are
 CC capable of producing higher levels of TAPS than their wild type
 CC counterparts. The present sequence represents a P. ciferrii ribosomal
 CC protein encoded by the L41 gene

XX SQ Sequence 106 AA;

Query Match 85.5%; Score 490; DB 3; Length 106;
 Best Local Similarity 84.0%; Pred. No. 7.3e-51;
 Matches 89; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 MVNVPKTRTYCKGKCKKHTPHKVTQYKKGDSIFAQGRYDRKQSGYGQTKPVFHK 60
 Db 1 MVNVPKTRTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKQSGYGQTKPVFHK 60
 Qy 61 KAKTTKKVLRLECSVCCKYKQMTLKRCKHFGELGDKTKGAATSF 106
 Db 61 KAKTTKKVLRLECVCKTKAQLAKRCKHFGELGDKTKGQALQF 106

RESULT 5
 AAW57490
 ID AAW57490 standard; protein; 106 AA.

XX AC AAW57490;
 XX DT 17-OCT-2003 (revised)
 XX DT 14-AUG-1998 (first entry)
 XX DE Amino acid sequence of ragment containing L41 gene.
 XX KW Candida utilis; yeast vector; promoter; marker gene; GAP gene;
 XX KW high-efficiency integration; monellin; food; drug; L41; URA3.
 XX OS Pichia jadinii.
 XX PN WO9807873-A1.
 XX PD 26-FEB-1998.
 XX PF 22-AUG-1997; 97WO-JP002924.
 XX PR 23-AUG-1996; 96JP-00241062.
 XX (KIRI) KIRIN BEER KK.
 XX Kondo K, Miura Y;
 XX WPI; 1998-169177/15.
 DR N-PSDB; AAV31513.
 XX Yeast vector for multi-copying on to chromosomes of yeast such as Candida
 PT utilis - contains a shortened promoter sequence linked to a marker gene
 PT for high-efficiency integration.
 XX Example; Fig 10; 107pp; Japanese.
 XX This is the amino acid sequence of the fragment containing yeast L41
 CC gene. This can be used in the construction of a yeast vector for multi-
 CC copying on to chromosomes of yeast such as Candida utilis. The vector
 CC contains a DNA homologous with a chromosomal gene of the yeast

CC (preferably ribosomal DNA (rDNA) such as the URA3, L41, PGK, GAP or PMA
 CC gene), a marker gene to be used in transformant selection (such as a drug
 CC resistance gene, e.g. the cycloheximide resistance gene L41, the G418
 CC resistance gene Tn903-APT, or the hygromycin B resistance gene (from
 CC E.coli) HPT), a shortened promoter sequence such as the C-utilis L41,
 CC phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dihydrogenase
 CC (GAP) or plasma membrane proton ATPase (PMA) gene promoter and a gene of
 CC interest from yeast or other origin. The vectors are useful in the
 CC preparation of proteins for food or drug use in high efficiency. They can
 CC be used especially for the production of single-chain monellin, which is
 CC a low-calorie sweetener whose thermostability is greater than that of the
 CC dimeric natural monellin. Multiple copies of the desired gene are
 CC integrated into the yeast chromosome and high expression efficiency is
 CC obtained. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 106 AA;

Query Match 84.3%; Score 483; DB 2; Length 106;
 Best Local Similarity 84.0%; Pred. No. 5.1e-50;
 Matches 89; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MWNVPTRTTYCKGKAKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60
 DB 1 MWNVPTRTTYCKGKAKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60
 QY 61 KAKTTKKVLRLECVCKYKQMOTLKRCKHPELGGDKTKTGAAISF 106
 DB 61 KAKTTKKVLRLECVCKYKQMOTLKRCKHPELGGDKTKTGAAISF 106

RESULT 6

ADCS8117

ID ADCS8117 standard; protein; 106 AA.

XX

AC ADCS8117;

DT 01-JAN-2004 (first entry)

XX Ribosomal protein similar to FCWP1 #333.

DE

XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
 KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
 KW Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;
 KW Macrophoma; Mycosphaerella; Nectria; Peronospora; Phoma;
 KW Phymatotrichum; Phytophthora; Plasmodiopsis; Podosphaera; Puccinia; Puthium;
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
 KW Septoria; Thielaviopsis; Venturia; Verticillium.

XX Unidentified.

XX US6573361-B1.

XX 03-JUN-2003.

XX 07-DEC-2000; 2000US-00732210.

XX 07-DEC-1999; 99US-0169340P.

XX 07-DEC-1999; 99US-0169513P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;

XX WPI; 2003-754558/71.

XX Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
 PT for controlling fungal infections in plants.
 PT Example 21; SEQ ID NO 370; 27pp; English.
 PS The invention relates to an isolated antifungal ribosomal protein from
 CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein AlyAPP from Alyseum and FCWP1,

CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by Alternaria (e.g. Alternaria brassicola, Alternaria solani),
 CC Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea),
 CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
 CC Colletotrichum (e.g. Colletotrichum indumethianum), Diplodia (e.g.
 CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
 CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
 CC moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces
 CC graminis f. sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
 CC (e.g. Macrophoma phaseolina, Meganapothia grisea), Mycosphaerella
 CC (e.g. Mycosphaerella figliensis), Nectria (Nectria haematococca), Phoma
 CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
 CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
 CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
 CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
 CC citrophthora, Phytophthora megasperma f. sp. sojae, Phytophthora
 CC infestans), Plasmodiopsis (e.g. Plasmodiopsis viticola), Podosphaera (e.g.
 CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghii, Puccinia
 CC striformis, Puccinia graminis f. sp. tritici, Puccinia asparagi,
 CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
 CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
 CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
 CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
 CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
 CC Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora
 CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
 CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
 CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
 CC Verticillium albo-atrum). Mutations in the proteolytic consensus
 CC sequences contained within FCWP1 provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWP1. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX Sequence 106 AA;

Query Match 84.3%; Score 483; DB 7; Length 106;

Best Local Similarity 82.1%; Pred. No. 5.1e-50;

Matches 87; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MWNVPTRTTYCKGKAKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

DB 1 MWNVPTRTTYCKGKAKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

QY 61 KAKTTKKVLRLECVCKYKQMOTLKRCKHPELGGDKTKTGAAISF 106

DB 61 KAKTTKKVLRLECVCKYKQMOTLKRCKHPELGGDKTKTGAAISF 106

RESULT 7

AAG70870

ID AAG70870 standard; protein; 106 AA.

XX

AC AAG70870;

XX

DT 27-JUL-2001 (first entry)

XX

DE C albicans apoptosis associated protein #50.

XX

KW Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;

KW autoimmune disease; ischaemia; neurodegeneration.

XX

OS Candida albicans.

XX

PN WO200102550-A2.

XX

DT 11-JAN-2001.

PD

XX 03-JUL-2000; 2000WO-BE000077.
 XX 01-JUL-1999; 99EP-00870141.
 XX (JANC) JANSSEN PHARM NV.
 XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
 XX Nelissen BJM, Reekmans RJ;
 XX WPI; 2001-367042/38.
 XX N-PSDB; AAH29906.
 XX Yeast and fungal nucleic acids encoding proteins involved in a pathway
 PT leading to programmed cell death, useful for treating proliferative
 PT disorders, yeast and fungal infections, or for preventing apoptosis in
 PT certain diseases.
 XX Claim 24; Fig 2; 218pp; English.
 XX The present invention provides the protein and coding sequences of a
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*
 CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify
 CC treatments for fungal and yeast infections, for proliferative diseases
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
 CC and neurodegeneration. The present sequence is one of the *C. albicans*
 CC proteins of the invention
 XX Sequence 106 AA;
 XX Query Match 84.1%; Score 482; DB 4; Length 106;
 XX Best Local Similarity 83.0%; Pred. No. 6.7e-50;
 XX Matches 88; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MNNVPKTRRTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKOSGYGGQTKPVPHK 60
 DB 1 MNNVPKTRKTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKOSGYGGQTKQIPHK 60
 QY 61 KAKTTKKVLRLECSVCVKYKQMTLKRCKHFLGDKKTKGAATSF 106
 DB 61 KAKTTKKVLRLECSVCVKYKQMTLKRCKHFLGDKKTKGAATSF 106
 RESULT 8
 ID AAG70742
 XX AAG70742 standard; protein; 106 AA.
 AC AAG70742;
 XX 27-JUL-2001 (first entry)
 XX *S. cerevisiae* apoptosis associated protein YHR021C.
 XX Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;
 KW autoimmune disease; ischaemia; neurodegeneration.
 XX *Saccharomyces cerevisiae*.
 XX W0200102550-A2.
 XX 11-JAN-2001.
 XX 03-JUL-2000; 2000WO-BE000077.
 XX 01-JUL-1999; 99EP-00870141.
 XX (JANC) JANSSEN PHARM NV.
 XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
 XX Nelissen BJM, Reekmans RJ;
 XX WPI; 2001-367042/38.
 XX N-PSDB; AAH29778.

XX Yeast and fungal nucleic acids encoding proteins involved in a pathway
 PT leading to programmed cell death, useful for treating proliferative
 PT disorders, yeast and fungal infections, or for preventing apoptosis in
 PT certain diseases.
 XX Claim 1; Fig 1; 218pp; English.
 XX The present invention provides the protein and coding sequences of a
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*
 CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify
 CC treatments for fungal and yeast infections, for proliferative diseases
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
 CC and neurodegeneration. The present sequence is one of the *S. cerevisiae*
 CC proteins of the invention
 XX Sequence 106 AA;
 XX Query Match 83.9%; Score 481; DB 4; Length 106;
 XX Best Local Similarity 82.1%; Pred. No. 8.8e-50;
 XX Matches 87; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MNNVPKTRRTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKOSGYGGQTKPVPHK 60
 DB 1 MNNVPKTRKTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKOSGYGGQTKPVPHK 60
 QY 61 KAKTTKKVLRLECSVCVKYKQMTLKRCKHFLGDKKTKGAATSF 106
 DB 61 KAKTTKKVLRLECSVCVKYKQMTLKRCKHFLGDKKTKGAATSF 106
 RESULT 9
 ID ADC88813
 XX ADC88813 standard; protein; 102 AA.
 AC ADC88813;
 XX 01-JAN-2004 (first entry)
 XX Ribosomal protein similar to FCWP1 #1029.
 XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
 KW plant fungal infection; Alternaria; Ascochyta; Cercospora;
 KW *Colletotrichum*; *Diplodia*; *Fusarium*; *Gaeumannomyces*; *Helminthosporium*;
 KW *Macrophomina*; *Mycosphaerella*; *Nectria*; *Peronospora*; *Phoma*;
 KW *Phymatotrichum*; *Phytophthora*; *Plasmopara*; *Podosphaera*; *Puccinia*; *Puthium*;
 KW *Pyrenophora*; *Pyrularia*; *Pythium*; *Rhizoctonia*; *Sclerotium*; *Sclerotinia*;
 KW *Septoria*; *Thielaviopsis*; *Venturia*; *Verticillium*.
 XX Unidentified.
 XX US6573361-B1.
 XX 03-JUN-2003.
 XX 07-DEC-2000; 2000US-00732210.
 XX 07-DEC-1999; 99US-0169340P.
 XX 07-DEC-1999; 99US-0169513P.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
 XX WPI; 2003-754558/71.
 XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful
 PT for controlling fungal infections in plants.
 XX Example 21; SEQ ID NO 1066; 27pp; English.
 XX The invention relates to an isolated antifungal ribosomal protein from
 CC *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the

CC signal peptide of the antifungal protein AlyAPP from *Alyseum* and FCWP1,
 CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by *Alternaria* (e.g. *Alternaria brassicicola*, *Alternaria solani*),
 CC *Ascochyta* (e.g. *Ascochyta pisi*), *Botrytis* (e.g. *Botrytis cinerea*),
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,
 CC *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium solani*, *Fusarium*
 CC *moniliforme*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*
 CC *graminis* f.sp. *tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*
 CC *graminis* f.sp. *tritici*), *Helminthosporium maydis*), *Macrophomina*
 CC (e.g. *Macrophomina phaseolina*, *Magnaporthe grisea*), *Mycosphaerella*
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*), *Phoma*
 CC *peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*
 CC *citrophthora*, *Phytophthora megasperma* f.sp. *sojae*, *Phytophthora*
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*
 CC *striformis*, *Puccinia graminis* f.sp. *tritici*, *Puccinia asparagi*,
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puccinia* (e.g. *Puccinia*
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),
 CC *Pyricularia* (e.g. *Pyricularia oryzae*), *Pythium* (e.g. *Pythium ultimum*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stragonospora*
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus
 CC sequences contained within FCWP1 provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWP1. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.
 CC
 XX
 SQ Sequence 102 AA;

Query Match 83.4%; Score 478; DB 7; Length 102;
 Best Local Similarity 86.3%; Pred. No. 1.9e-49;
 Matches 88; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 VNVPTRTYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 61

Db 1 VNVPTRTYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

QY 62 AKTTKKVLRLECSVCKYKQMTLKRCKHFELGGDKTKGAA 103

Db 61 AKTTKKVLRLECSVCKYKQMTLKRCKHFELGGDKTKGAA 102

RESULT 10

AAG70795

ID AAG70795 standard; protein; 116 AA.

AC AAG70795;

XX 27-JUL-2001 (first entry)

DE S cerevisiae apoptosis associated protein YNL096C.

XX Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;

KW autoimmune disease; ischaemia; neurodegeneration.

XX Saccharomyces cerevisiae.

OS WO200102550-A2.

XX

PD 11-JAN-2001.

XX 03-JUL-2000; 2000WO-BE000077.

XX 01-JUL-1999; 99BP-00870141.

XX (JANC) JANSSEN PHARM NV.

XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;

PI Nelissen BJM, Reekmans RJ;

XX WPI; 2001-367042/38.

DR N-PSDB; AAH29831.

XX Yeast and fungal nucleic acids encoding proteins involved in a pathway

PT leading to programmed cell death, useful for treating proliferative

PT disorders, yeast and fungal infections, or for preventing apoptosis in

PT certain diseases.

XX Claim 1; Fig 1; 218pp; English.

XX The present invention provides the protein and coding sequences of a

CC number of apoptosis associated proteins from the yeast *Saccharomyces*

CC cerevisiae and the fungus *Candida albicans*. These can be used to identify

CC treatments for fungal and yeast infections, for proliferative diseases

CC and for apoptosis related diseases such as autoimmune diseases, ischaemia

CC and neurodegeneration. The present sequence is one of the *S. cerevisiae*

CC proteins of the invention

XX Sequence 116 AA;

Query Match 83.4%; Score 478; DB 4; Length 116;

Best Local Similarity 81.1%; Pred. No. 2.3e-49;

Matches 86; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNVPKTRTYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

Db 11 LVNVPKTRTYCKGKCKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 70

QY 61 KAKTTKKVLRLECSVCKYKQMTLKRCKHFELGGDKTKGAAISF 106

Db 71 KAKTTKKVLRLECSVCKYKQMTLKRCKHFELGGDKTKGAAISF 116

RESULT 11

ADC88816

ID ADC88816 standard; protein; 105 AA.

XX AC ADC88816;

XX 01-JAN-2004 (first entry)

XX Ribosomal protein similar to FCWP1 #1032.

XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;

KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;

KW Colletotrichum; Diplodia; Fusarium; Gaeumannomyces; Helminthosporium;

KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;

KW Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;

KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;

KW Septoria; Thielaviopsis; Venturia; Verticillium.

XX Unidentified.

XX US6573361-B1.

XX 03-JUN-2003.

XX 07-DEC-2000; 2000US-00732210.

XX 07-DEC-1999; 99US-0169340P.

XX 07-DEC-1999; 99US-0169513P.

XX

PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
 XX WPI; 2003-754558/71.
 XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful
 XX for controlling fungal infections in plants.
 XX Example 21; SEQ ID NO 1069; 27pp; English.
 XX The invention relates to an isolated antifungal ribosomal protein from
 CC *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein AlyAPP from *Alyssum* and FCWP1,
 CC encoded by the nucleic acid appearing as ADC8758. The FCWP1 proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by *Alternaria* (e.g. *Alternaria brassicola*, *Alternaria solani*),
 CC *Ascochyta* (e.g. *Ascochyta pisi*); *Botrytis* (e.g. *Botrytis cinerea*),
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,
 CC *Fusarium graminearum*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*
 CC *graminis f.sp. tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*
 CC *graminis f.sp. tritici*), *Helminthosporium maydis*), *Macrophomina*
 CC (e.g. *Macrophomina phaseolina*, *Maganaporthe grisea*), *Mycosphaerella*
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*),
 CC *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*
 CC *citrophthora*, *Phytophthora megasperma f.sp. sojae*, *Phytophthora*
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*
 CC *striformis*, *Puccinia graminis f.sp. tritici*, *Puccinia asparagi*,
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia oryzae*), *Pythium* (e.g. *Pythium ultimum*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stagonospora*
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus
 CC sequences contained within FCWP1 provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWP1. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=6573361B1.
 XX Seq Sequence 105 AA;
 Query Match 83.1%; Score 476; DB 7; Length 105;
 Best Local Similarity 81.9%; Pred. No. 3.5e-49;
 Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 VNVPKTRTYCKGKCKKHTPHKTYQYKKGDSIFAGKRRYDRKQSGYGGQTKPVFHK 61
 Db VNVPKTRTYCKGKCKKHTPHKTYQYKKGDSIFAGKRRYDRKQSGYGGQTKPVFHK 60
 QY 62 AKTKKVVLECSVCKVQMTLKRCKHPFELGDKTKGAATSF 106
 Db AKTKKVVLECSVCKVQMTLKRCKHPFELGDKTKGAATSF 105
 RESULT 12
 ADC88805
 ID ADC88805 standard; protein; 105 AA.
 XX

AC ADC88805;
 XX 01-JAN-2004 (first entry)
 XX Ribosomal protein similar to FCWP1 #1021.
 XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
 KW plant fungal infection; *Alternaria*; *Ascochyta*; *Botrytis*; *Cercospora*;
 KW *Colletotrichum*; *Diplodia*; *Fusarium*; *Gaeumannomyces*; *Helminthosporium*;
 KW *Macrophomina*; *Mycosphaerella*; *Nectria*; *Peronospora*; *Phoma*;
 KW *Phymatotrichum*; *Phytophthora*; *Plasmopara*; *Podosphaera*; *Puccinia*; *Puthium*;
 KW *Pyrenophora*; *Pycularia*; *Pythium*; *Rhizoctonia*; *Sclerotium*; *Sclerotinia*;
 KW *Septoria*; *Thielaviopsis*; *Venturia*; *Verticillium*.
 XX Unidentified.
 XX US6573361-B1.
 XX 03-JUN-2003.
 XX 07-DEC-2000; 2000US-00732210.
 XX 07-DEC-1999; 99US-0169340P.
 XX 07-DEC-1999; 99US-0169513P.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
 XX WPI; 2003-754558/71.
 XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful
 XX for controlling fungal infections in plants.
 XX Example 21; SEQ ID NO 1058; 27pp; English.
 XX The invention relates to an isolated antifungal ribosomal protein from
 CC *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein AlyAPP from *Alyssum* and FCWP1,
 CC encoded by the nucleic acid appearing as ADC8758. The FCWP1 proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by *Alternaria* (e.g. *Alternaria brassicola*, *Alternaria solani*),
 CC *Ascochyta* (e.g. *Ascochyta pisi*); *Botrytis* (e.g. *Botrytis cinerea*),
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,
 CC *Fusarium graminearum*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*
 CC *graminis f.sp. tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*
 CC *graminis f.sp. tritici*), *Helminthosporium maydis*), *Macrophomina*
 CC (e.g. *Macrophomina phaseolina*, *Maganaporthe grisea*), *Mycosphaerella*
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*),
 CC *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*
 CC *citrophthora*, *Phytophthora megasperma f.sp. sojae*, *Phytophthora*
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*
 CC *striformis*, *Puccinia graminis f.sp. tritici*, *Puccinia asparagi*,
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia oryzae*), *Pythium* (e.g. *Pythium ultimum*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stagonospora*
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus
 CC sequences contained within FCWP1 provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWP1. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=6573361B1.

CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWPI. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX SQ Sequence 105 AA;

Query Match 82.2%; Score 471; DB 7; Length 105;
 Best Local Similarity 81.0%; Pred. No. 1.4e-48;
 Matches 85; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 2 VNVPKTRTYCKGKACKKHPTKHTQYKKGKDSIFAQGRYDRKQSGYGQTKPVPHKK 61

Db 1 VNVPKTRTYCKGKACKKHPTKHTQYKKGKDSIFAQGRYDRKQSGYGQTKPVPHKK 60

QY 62 AKTTKKVLLRLECSVCCKYKQMTLKRCKHPELGDKTKTGAAISF 106

Db 61 AKTTKKVLLRLECSVCCKYKQMTLKRCKHPELGDKTKTGAAISF 105

RESULT 13

ADC88810
 ID ADC88810 standard; protein; 105 AA.

XX AC ADC88810;

XX DT 01-JAN-2004 (first entry)

XX DE Ribosomal protein similar to FCWPI #1026.

XX KW Antifungal protein; ribosomal protein; FCWPI; AlyAPP;

XX KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;

XX KW Colletotrichum; Diplodia; Fusarium; Gaëmanomyces; Helminthosporium;

XX KW Macrophoma; Mycosphaerella; Nectria; Peronospora; Phoma;

XX KW Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;

XX KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;

XX KW Septoria; Thielaviopsis; Venturia; Verticillium.

XX OS Unidentified.

XX FN US6573361-B1.

XX PD 03-JUN-2003.

XX PF 07-DEC-2000; 2000US-00732210.

XX PR 07-DEC-1999; 99US-0169340P.

XX PR 07-DEC-1999; 99US-0169513P.

XX PA (MONS) MONSANTO TECHNOLOGY LLC.

XX PI Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;

XX DR WPI; 2003-754558/71.

XX PT Novel antifungal protein FCWPI, isolated from *Fusarium culmorum*, useful
 XX for controlling fungal infections in plants.

XX PS Example 21; SEQ ID NO 1063; 27pp; English.

XX The invention relates to an isolated antifungal ribosomal protein from
 CC *Fusarium culmorum*, FCWPI. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein AlyAPP from *Alyssum* and FCWPI,
 CC encoded by the nucleic acid appearing as ADC87758. The FCWPI proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by *Alternaria* (e.g. *Alternaria brassicicola*, *Alternaria solani*),
 CC *Ascochyta* (e.g. *Ascochyta pisi*); *Botrytis* (e.g. *Botrytis cinerea*),
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,
 CC *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium solani*, *Fusarium*
 CC *moniliforme*, *Fusarium roseum*), *Gaeumanomyces* (e.g. *Gaeumanomyces*

CC *graminis* f.sp. *tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*
 CC *Helminthosporium carbonum*, *Helminthosporium maydis*), *Macrophoma*
 CC (e.g. *Macrophoma phaseolina*, *Maganaportha grisea*), *Mycosphaerella*
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria heamatococca*), *Phoma*
 CC *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*
 CC *citrophthora*, *Phytophthora megasperma* f.sp. *sojae*, *Phytophthora*
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*
 CC *striiformis*, *Puccinia graminis* f.sp. *tritici*, *Puccinia asparagi*,
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),
 CC *Pyricularia* (e.g. *Pyricularia oryzae*), *Pythium* (e.g. *Pythium ultimum*),
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria tritici*), *Stagonospora*
 CC *nodorum* / *Phaeosphaeria nodorum*, *Uncinula* (e.g. *Uncinula necator*), *Venturia*
 CC *Thielaviopsis basicola*), *Verticillium* (e.g. *Verticillium dahliae*,
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus
 CC sequences contained within FCWPI provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>7) and molecular weight (<20kDa) to FCWPI, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWPI. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX SQ Sequence 105 AA;

Query Match 80.8%; Score 463; DB 7; Length 105;

Best Local Similarity 79.0%; Pred. No. 1.3e-47;

Matches 83; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 2 VNVPKTRTYCKGKACKKHPTKHTQYKKGKDSIFAQGRYDRKQSGYGQTKPVPHKK 61

Db 1 VNVPKTRTYCKGKACKKHPTKHTQYKKGKDSIFAQGRYDRKQSGYGQTKPVPHKK 60

QY 62 AKTTKKVLLRLECSVCCKYKQMTLKRCKHPELGDKTKTGAAISF 106

Db 61 AKTTKKVLLRLECSVCCKYKQMTLKRCKHPELGDKTKTGAAISF 105

RESULT 14

AAR32293
 ID AAR32293 standard; protein; 106 AA.

XX AC AAR32293;

XX DT 25-MAR-2003 (revised)

XX DT 08-JUN-1993 (first entry)

XX DE Sequence of ribosomal resistance protein A which confers resistant to
 XX cycloheximide.

XX KW Cycloheximide resistance protein; protein A; ribosomal protein.

XX OS *Kluyveromyces lactis*.

XX FN W09302201-A1.

XX PD 04-FEB-1993.

XX PF 15-JUL-1992; 92WO-FR000685.

XX PR 15-JUL-1991; 91FR-00008906.

XX PA (INSP) INST PASTEUR.

XX PI Dehoux P, Davies J;

XX WPI; 1993-058797/07.
 XX
 XX New nucleic acid fragment imparting resistance to cycloheximide -
 PT isolated from Kluyveromyces lactis, useful as selection marker for DNA
 PT transfer in eukaryotic cells.
 XX
 XX Claim 11; Fig 4; 42pp; French.
 XX
 XX DNA sequence I encodes a 106 AA ribosomal resistance protein. It is
 CC derived from Kluyveromyces fragilis. The protein confers resistance to
 CC cycloheximide (Ch) at over 1mg/ml in both K. lactis and Saccharomyces
 CC cerevisiae. DNA sequence II encodes the resistance protein and a
 CC cofactor. The open reading frame of DNA sequence II extends from bases 1-
 CC 1560; it contains 2 exons 629-632 and 1223-1539 and includes the gene
 CC promoter. The co-factor is encoded by region 1561-2740. Cells transformed
 CC with the nucleic acid sequences become resistant to Ch and so the
 CC sequences can be used as a selection marker for controlling the transfer
 CC of nucleic acid. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 106 AA;
 XX
 XX Query Match 80.6%; Score 462; DB 2; Length 106;
 XX Best Local Similarity 78.3%; Pred. No. 1.7e-47;
 XX Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 XX
 Qy 1 MNVVPKTRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGGQTKPVFHK 60
 Db 1 MNVVPKTRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGGQTKPVFHK 60
 Qy 61 KAKTTKVVLRLECSVCYKQWMTLKRCKHFKELGDKTKTGAAISF 106
 Db 61 KAKTTKVVLRLECSVCYKQWMTLKRCKHFKELGDKTKTGAAISF 106
 RESULT 15
 AD88118
 ID AD88118 standard; protein; 105 AA.
 XX
 XX AC AD88118;
 XX
 XX 01-JAN-2004 (first entry)
 XX
 XX Ribosomal protein similar to FCWPI #334.
 DE
 XX Antifungal protein; ribosomal protein; FCWPI; AlyAPP;
 KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
 KW Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;
 KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
 KW Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotinia; Sclerotium;
 KW Septoria; Thielaviopsis; Venturia; Verticillium.
 XX
 OS Unidentified.
 XX
 XX US6573361-B1.
 XX
 XX 03-JUN-2003.
 XX
 XX 07-DEC-2000; 2000US-00732210.
 XX
 XX 07-DEC-1999; 99US-0169340P.
 XX
 XX 07-DEC-1999; 99US-0169513P.
 XX
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
 XX WPI; 2003-754558/71.
 XX
 XX Novel antifungal protein FCWPI, isolated from Fusarium culmorum, useful
 PT for controlling fungal infections in plants.
 XX

PS
 XX

Example 21; SEQ ID NO 371; 27pp; English.

The invention relates to an isolated antifungal ribosomal protein from
 fusarium culmorum, FCWPI. Also included is a fusion protein between the
 signal peptide of the antifungal protein AlyAPP from Alyseum and FCWPI,
 encoded by the nucleic acid appearing as A0887758. The FCWPI proteins are
 useful for controlling fungal infections in plants, such as those caused
 by Alternaria (e.g. Alternaria brassicicola, Alternaria solani),
 Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea),
 Cercospora (e.g. Cercospora kikuchii, Cercospora zae-maydis),
 Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
 Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
 Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
 moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces
 graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
 graminis f.sp. tritici), Helminthosporium maydis), Macrophomina
 (e.g. Macrophomina phaseolina, Maganaporthe grisea), Mycosphaerella
 (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca),
 Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
 (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
 Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
 Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
 citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora
 infestans), Plasmopara (e.g. Plasmopara viticola), Podosphaera (e.g.
 Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia
 striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,
 Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
 aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentum),
 Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
 Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
 (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
 Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora
 nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
 Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
 (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
 Verticillium albo-atrum). Mutations in the proteolytic consensus
 sequences contained within FCWPI provides improved stability of its
 antifungal activity. Also disclosed are ribosomal proteins with similar
 PI (>7) and molecular weight (<20kDa) to FCWPI, which may act as
 antifungal proteins. The present sequence represents one of the ribosomal
 proteins similar to FCWPI. Note: The sequence data for this patent did
 not form part of the printed specification, but was obtained in
 electronic format directly from USPTO at
 seqdata.uspto.gov/sequence.html?DocID=6573361B1.

Sequence 105 AA;

Query Match 80.5%; Score 461; DB 7; Length 105;
 Best Local Similarity 78.1%; Pred. No. 2.2e-47;
 Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 Qy 2 VNVPKTRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGGQTKPVFHK 61
 Db 1 VNVPKTRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGGQTKPVFHK 60
 Qy 62 AKTTKVVLRLECSVCYKQWMTLKRCKHFKELGDKTKTGAAISF 106
 Db 61 AKTTKVVLRLECSVCYKQWMTLKRCKHFKELGDKTKTGAAISF 105

Search completed: January 18, 2005, 20:14:04
 Job time : 287 secs

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 08:40:39 ; Search time 448.315 Seconds
(without alignments)
8676.543 Million cell updates/sec

Title: US-09-830-691A-4
Perfect score: 741
Sequence: 1 ctgagtggcgtggaat.....ataactgtgtaattctaga 741

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	739	99.7	741	3	AA15569 Phaffia r
2	152	20.5	1904	2	AAV60108 Rhizocton
3	150.4	20.3	1793	2	AAV60107 Rhizocton
4	145.4	19.6	1247	10	ACA61067 Phyllosti
5	142	19.2	9558	2	AAQ88228 Valencia
6	140	18.9	913	11	ADM45469 Insect re
7	138.2	18.7	1821	2	AAV54087 Nucleotid
8	136	18.4	1734	5	ABK49559 Putrefact
9	134.6	18.2	5373	2	AAV31379 Arabidops
10	134.6	18.2	59590	3	AAF22281 BAC conta
11	132.2	17.8	3172	10	ADF54865 Ribosomal
12	131.6	17.8	703	2	ADR01486 A. gossyp
13	131.6	17.8	706	2	ADR02122 A. gossyp
14	131.6	17.8	717	2	ADR01910 A. gossyp
15	130	17.5	712	2	ADR02218 A. gossyp
16	130	17.5	2089	8	ABZ20764 Muscodor
17	128.4	17.3	1761	6	ABV78699 C. crassi
18	128.4	17.3	1766	6	ABV78720 C. sinens
19	128.4	17.3	1766	6	ABV78708 C. sinens
20	128.4	17.3	1766	6	ABV78714 C. sinens
21	128.4	17.3	1766	6	ABV78711 C. sinens

22	128.4	17.3	1766	6	ABV78717	Abv78717 C. sinens
23	128.4	17.3	1766	6	ABV78705	Abv78705 C. sinens
24	128.4	17.3	1766	6	ABV78702	Abv78702 C. sinens
25	128.4	17.3	1766	6	ABV78723	Abv78723 C. sinens
26	128.4	17.3	1771	2	AAV61668	AAV61668 Fusarium
27	126.8	17.1	568	3	AAF11545	AAF11545 Aspergill
28	126.2	17.0	1840	2	AAV54086	AAV54086 Nucleotid
c 29	125.6	17.0	3420	6	ABA99033	ABA99033 Saccharom
c 30	119.2	16.1	367	8	ABX43439	ABx43439 Bovine ES
c 31	119	16.1	570	3	AAF08498	AAF08498 Fusarium
32	118.6	16.0	2055	8	ABZ20766	ABz20766 Muscodor
33	117.8	15.9	873	11	ADM44838	Adm44838 Insect re
34	117	15.8	717	11	ADM45463	Adm45463 Insect re
35	117	15.8	1737	8	AA151417	AA151417 Spongibel
36	116.8	15.8	1776	4	AAF25849	AAF25849 S. exigui
37	115.4	15.6	617	3	AAF10913	AAF10913 Fusarium
38	114.6	15.5	1750	2	AAT90818	AAT90818 C. parvum
39	114.6	15.5	1750	3	AAA46368	AAA46368 Nucleotid
40	114.6	15.5	1798	4	AA14297	AA14297 Yeast DNA
41	114.6	15.5	1798	5	AA14004	AA14004 DNA to in
42	114.6	15.5	1802	5	AAF23018	AAF23018 Yeast 18S
c 43	113.6	15.3	723	2	ADR02260	ADR02260 A. gossyp
44	112.6	15.2	762	10	ADK54329	Adk54329 Plant DNA
45	112.6	15.2	1878	10	ADK57663	Adk57663 Plant DNA

ALIGNMENTS

RESULT 1
AA15569
ID AA15569 standard; DNA; 741 BP.
XX
AC AA15569;
XX
DT 15-SEP-2003 (revised)
DT 25-SEP-2000 (first entry)
XX
XX Phaffia rhodozyma rDNA gene.
XX
XX Yeast; ribosomal DNA; rDNA; non-transcription spacer; NTS;
XX selectable marker; ribosomal DNA; db.
XX Xanthophyllomyces dendrorhous.
OS
XX
XX WO200026387-A1.
XX
PD 11-MAY-2000.
XX
XX 29-MAY-1999; 99WO-KR000265.
XX
XX 31-OCT-1998; 98KR-00046547.
XX
XX (ROAD) KOREA ADV INST SCI & TECHNOLOGY.
PA (HAIT-) HAI TAI CONFECTIONERY CO LTD.
XX
XX Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;
PI Choi SK, Son YR;
XX
XX WPI; 2000-365630/31.
DR
XX
XX Novel vector comprising a cyclohexamide-resistance gene and a ribosomal
PT DNA useful for the transformation of Phaffia rhodozyma.
XX
XX Claim 5; Page 38-39; 43pp; English.
PS
XX
XX The present sequence is a Phaffia rhodozyma rDNA gene. This sequence can
CC be used to enhance the integration efficiency of foreign DNA into host
CC genomes. This is because the rDNA is highly repeated as tandem units in
CC eukaryotic genomes. This rDNA also has a non-transcription spacer (NTS),
CC i.e. a DNA spacer between transcribed DNA. This NTS may be used as a
CC component of a transforming vector, which also has a selectable marker
CC and a foreign gene. The wild-type Phaffia rhodozyma L41 gene, which

CC	encodes a ribosomal protein, has a proline residue at position 56. This residue is responsible for P. rhodozyma sensitivity to cyclohexamide. However, when this residue is mutated via site-directed mutagenesis to give rise to a glutamine at position 56, the yeast gains resistance to cyclohexamide. The modified I41 gene can be used as a selectable marker of a transforming vector for P. rhodozyma. The vector can be used, with the present sequence to early foreign DNA, e.g. the astaxanthin gene, a carotenoid. (Updated on 15-SEP-2003 to standardise OS field)
XX	Sequence 741 BP; 164 A; 175 C; 215 G; 185 T; 0 U; 2 Other;
SQ	Query Match 99.7%; Score 739; DB 3; Length 741;
	Best Local Similarity 100.0%; Pred. No. 9.3e-234;
	Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTCAGTGGACGGTGGCAATTCGTTGCTCGTTGGTGTCTCACTCGCAACCCAAAGCAGT 60
DB	1 CTCAGTGGACGGTGGCAATTCGTTGCTCGTTGGTGTCTCACTCGCAACCCAAAGCAGT 60
QY	61 CGCTTACCCGGGTAGCTCCGGGTGGCGCGATGATTGTTGGTGTGGATTCTTCCCTTA 120
DB	61 CGCTTACCCGGGTAGCTCCGGGTGGCGCGATGATTGTTGGTGTGGATTCTTCCCTTA 120
QY	121 TGGGTAGAACGACGCGCAACCAATCATTTGGAGAACCGCTCCGTTGTAGCCGACAGTCT 180
DB	121 TGGGTAGAACGACGCGCAACCAATCATTTGGAGAACCGCTCCGTTGTAGCCGACAGTCT 180
QY	181 GATTGATCAACATCGCAGCAGCTCCTCCGGACGGAGACTCGCGGGGATCGTACTCTATC 240
DB	181 GATTGATCAACATCGCAGCAGCTCCTCCGGACGGAGACTCGCGGGGATCGTACTCTATC 240
QY	241 TGGAAATCGCTGGCTCAATGGTAGTAGTCTTCACGATCGGCCATGAGGCGAGTCTAGGTGG 300
DB	241 TGGAAATCGCTGGCTCAATGGTAGTAGTCTTCACGATCGGCCATGAGGCGAGTCTAGGTGG 300
QY	301 GTTCGCTCGCGAAGACATGTGTGAGTGTCTGANNACATAATTGAGTACCGGGGATAGG 360
DB	301 GTTCGCTCGCGAAGACATGTGTGAGTGTCTGANNACATAATTGAGTACCGGGGATAGG 360
QY	361 CAAGCGGTGTTGTTGGTGGCGGTGGCTGTGAGCGAGTCTTGCTGCAAAAGCGATTCAATGCAC 420
DB	361 CAAGCGGTGTTGTTGGTGGCGGTGGCTGTGAGCGAGTCTTGCTGCAAAAGCGATTCAATGCAC 420
QY	421 CCCGGCTTGGCGACGCGCGCTGGTCAAGAAACACTAAACGGTTGACGCCATAAAGTAA 480
DB	421 CCCGGCTTGGCGACGCGCGCTGGTCAAGAAACACTAAACGGTTGACGCCATAAAGTAA 480
QY	481 TAAACACTCAAGTTTGTGTGGTCCGGGTGGGCTCTGTGCCCTGCGTGGGACCCGACGGGA 540
DB	481 TAAACACTCAAGTTTGTGTGGTCCGGGTGGGCTCTGTGCCCTGCGTGGGACCCGACGGGA 540
QY	541 GAGGAAAAAGTTCTGTGGCCCTCTCCTCTGTGGATAGTTACTGGTTGATCTCGCCAGTA 600
DB	541 GAGGAAAAAGTTCTGTGGCCCTCTCCTCTGTGGATAGTTACTGGTTGATCTCGCCAGTA 600
QY	601 GTCATATGCTTGTCTCAAGATTAGCCATGCATCTTAAGTATATAACAAATTCATACATG 660
DB	601 GTCATATGCTTGTCTCAAGATTAGCCATGCATCTTAAGTATATAACAAATTCATACATG 660
QY	661 TGAAATCGCAATGCGCTCAATTAAATCAGTTATAGTTTTATTTGATGGTACCTTGTCTACATG 720
DB	661 TGAAATCGCAATGCGCTCAATTAAATCAGTTATAGTTTTATTTGATGGTACCTTGTCTACATG 720
QY	721 GATAACTGTGGTAATTCCTAGA 741
DB	721 GATAACTGTGGTAATTCCTAGA 741

RESULT 2

AAV60108

ID AAV60108 standard; DNA; 1904 BP.

XX

AAV60108;

[illegible]

XX 28-FEB-1997; 97JP-00062106.
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 XX WPI; 1998-535035/46.
 XX Use of oligo:nucleotide for detecting or identifying fungus of
 XX Rhizoctonia genus - used to detect or identify fungus rapidly and
 XX exactly.
 XX Example 1; Page 8; 24pp; Japanese.
 XX The present sequence appears in the specification, which describes
 XX oligonucleotide probes for detecting or identifying of a fungus of
 XX Rhizoctonia genus. The sequences are derived from the 18s rRNA gene
 XX sequence, and are unique to Rhizoctonia species. (Updated on 17-OCT-2003
 XX to standardise OS field)
 XX Sequence 1793 BP; 460 A; 363 C; 463 G; 490 T; 0 U; 17 Other;
 XX
 Query Match 20.3%; Score 150.4; DB 2; Length 1793;
 Best Local Similarity 96.2%; Pred. No. 1.5e-38;
 Matches 154; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 582 CTGTTGATCTGCCAGTAGTCATATGCTTCTCTCAAGATTAAGCCATGCTCTAAG 641
 Db 1 CTGTTGATCTGCCAGTAGTCATATGCTTCTCTCAAGATTAAGCCATGCTCTAAG 60
 Qy 642 TATAACAAATTCATCTGGAACCTGCAATGCTCAATTAATCAGTTATATTT 701
 Db 61 TATAACAACTTTTGTACTGTGGAACCTGCAATGCTCAATTAATCAGTTATATTT 120
 Qy 702 GATGTAATCTTGTACATGATGTAATCTGTTGTAATTTCTAGA 741
 Db 121 GATGTAATCTTGTACATGATGTAATCTGTTGTAATTTCTAGA 160
 RESULT 4
 ID ACA61067 standard; DNA; 1247 BP.
 AC ACA61067;
 DT 14-JUL-2003 (first entry)
 DE Phyllosticta ribosomal DNA intergenic sequence (IGS).
 KW Guignardia; pathogen; internal transcribed spacer; ITS; citrus fruit;
 KW intergenic sequence; intronic sequence; calmodulin; chitin synthase;
 KW citrus blackspot; phyllosticta; intergenic sequence; IGS; ds.
 OS Phyllosticta sp.
 XX WO2003031933-A2.
 XX 17-APR-2003.
 XX 09-OCT-2002; 2002WO-US032227.
 XX 09-OCT-2001; 2001US-0327982P.
 XX (UYOR-) UNIV OREGON.
 XX Carroll GC;
 XX WPI; 2003-372133/35.
 XX Differentiating pathogenic and non-pathogenic Guignardia sp., by
 XX assessing hybridization between DNA from Guignardia- infected citrus and
 XX probes based on intronic sequences from calmodulin and chitin synthase
 XX genes.

PS Example 2; Fig 3; 37pp; English.
 XX The invention describes a method of differentiating pathogenic and non-
 XX pathogenic species of Guignardia (I). The method comprises obtaining a
 XX DNA sample from a citrus fruit infected with (I), immobilising the DNA,
 XX probing the immobilised DNA with a probe based on intergenic sequences
 XX and intronic sequences from within the calmodulin and chitin synthase
 XX genes, and demonstrating hybridisation with the probes to represent the
 XX pathogenic species and non-pathogenic species. The method is specific,
 XX rapid and useful for differentiating pathogenic species (e.g. Guignardia
 XX citricarpa, the causative agent of citrus blackspot) from non-pathogenic
 XX species of Guignardia. This sequence represents a phyllosticta ribosomal
 XX DNA intergenic sequence used to examine if ribosomal DNA intergenic
 XX sequences are species-specific and can therefore be used to differentiate
 XX between pathogenic and non-pathogenic species of Guignardia
 XX
 SQ Sequence 1247 BP; 253 A; 336 C; 352 G; 306 T; 0 U; 0 Other;
 XX
 Query Match 19.6%; Score 145.4; DB 10; Length 1247;
 Best Local Similarity 90.7%; Pred. No. 5.8e-37;
 Matches 166; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
 Qy 559 CCCTCTCCTCTGTCGATAGTTACCTGTTGATCTGTCGAGTAGTCATATGCTTGTCTCAA 618
 Db 450 CCCTGCGGCTCAAGATAGTTACCTGTTGATCTGTCGAGTAGTCATATGCTTGTCTCAA 509
 Qy 619 AGATTAAAGCCATGATGCTCTAAGTATATAACAAATTCATCTGTGAACTGCGAATGGCTC 678
 Db 510 AGATTAAAGCCATGATGCTCTAAGTATATAAGC-AACTATATCTGTAAGCTGCGAATGGCTC 568
 Qy 679 ATTAAATCAGTTATAGTTTATTTGATGCTGTCCTTGTGATGATGATGATGATGATGATGAT 738
 Db 569 ATTAAATCAGTTATAGTTTATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 628
 Qy 739 AGA 741
 Db 629 AGA 631
 RESULT 5
 ID AAQ88228 standard; DNA; 9558 BP.
 AC AAQ88228;
 DT 27-AUG-2003 (revised)
 DT 24-NOV-1995 (first entry)
 XX Valencia orange ribosomal RNA gene.
 DE Ribosomal RNA; rRNA; 18S; 28S; 5.8S; Valencia orange; RFLP analysis;
 KW DNA fingerprinting; restriction fragment length polymorphism; ds.
 OS Citrus.
 XX
 Key Location/Qualifiers
 FT misc_RNA 1..1597
 FT /*tag= a
 FT /product= "18S_rRNA"
 FT 1598..1848
 FT /*tag= b
 FT /function= "spacer"
 FT 1849..2011
 FT /*tag= c
 FT /product= "5.8S_rRNA"
 FT 2012..2238
 FT /*tag= d
 FT /function= "spacer"
 FT 2239..5582
 FT /*tag= e
 FT /product= "28S_rRNA"
 FT 5583..9396
 FT /*tag= f

XX JPI0234399-A.
 XX PN
 XX 08-SEP-1998.
 XX PD
 XX 28-FEB-1997; 97JP-00062114.
 XX PF
 XX 28-FEB-1997; 97JP-00062114.
 XX PR
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 XX PA
 XX WPI; 1998-535049/46.
 XX DR
 XX
 XX New oligo-nucleotide probe - for rapid and precise detection and
 XX PT identification of Pythium genus fungus.
 XX PT
 XX Disclosure; Page 9; 22pp; Japanese.
 XX PS
 XX This is the nucleotide sequence of the Pythium spinosum OPA-1 used in the
 XX CC method of the invention where novel probes are used for the detection and
 XX CC identification of a fungus of Pythium genus
 XX CC
 XX Sequence 1821 BP; 460 A; 329 C; 466 G; 518 T; 0 U; 48 Other;
 XX SQ

Query Match 18.7%; Score 138.2; DB 2; Length 1821;
 Best Local Similarity 91.2%; Pred. No. 1.7e-34;
 Matches 146; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 582 CTGTTGATCTGCCAGTAGTCATATGCTTCTCAAGATTAAAGCCATGCTCTAAG 641
 Db 1 CTGTTGATCTGCCAGTAGTCATATGCTTCTCAAGATTAAAGCCATGCTCTAAG 60

Qy 642 TATAACAAATTCATCTGCGAACTGCGAATGCTCAATTAAGTATAGTTATTT 701
 Db 61 TATAACAAATTTGCTACTGTGAACTGCGAATGCTCAATTAAGTATAGTTATTT 120

Qy 702 GATGCTACTTGTACATGATGTAATCTGTTGTAATCTAGA 741
 Db 121 GATAGTACCTTACTTGTGTAATCTGTAATCTAGA 160

RESULT 8
 ABK49559
 ID ABK49559 standard; DNA; 1734 BP.
 AC
 AC ABK49559;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 DE
 XX Putrefactive microbe associated polynucleotide.
 XX
 XX Putrefactive microbe; halotolerant; manganese peroxidase;
 KW paper-pulp industry; dyeing industry; industrial waste treatment; ds.
 XX
 XX Phlebia sp.
 OS
 XX JP2001169775-A.
 XX PN
 XX 26-JUN-2001.
 XX PD
 XX 06-OCT-2000; 2000JP-00307045.
 XX PF
 XX 06-OCT-1999; 99JP-00285955.
 XX PR
 XX (MEIJ) MEIJI SEIKA KAISHA LTD.
 XX PA
 XX WPI; 2001-608873/70.
 XX DR
 XX New microbe for decomposing substances and bleaching pulps, comprises a
 XX FT microbe that produces halotolerant manganese peroxidase.
 XX FT
 XX Claim 4; Page 9; 11pp; Japanese.
 XX PS
 XX

CC The invention describes a white putrefactive microbe having halotolerant
 CC manganese peroxidase activity. The microbe strain can be used in the
 CC paper-pulp industry, dyeing industry, and process of treating industrial
 CC waste. This sequence represents a putrefactive microbe associated
 CC polynucleotide. Note: This sequence does not encode the peptide shown in
 CC AAU79900
 XX
 SQ Sequence 1734 BP; 444 A; 348 C; 467 G; 475 T; 0 U; 0 Other;
 XX

Query Match 18.4%; Score 136; DB 5; Length 1734;
 Best Local Similarity 96.5%; Pred. No. 9e-34;
 Matches 139; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 598 GTAGTCATATGCTTGTCTCAAGATTAAAGCCATGCTCTAAGTATATAACAAATTCATA 657
 Db 1 GTAGTCATATGCTTGTCTCAAGATTAAAGCCATGCTCTAAGTATATAACAAAGTTTCTA 60

Qy 658 CTGTGAACTGCGAATGCTCAATTAAGTATAGTTATTTGATGCTACCTTGCTAC 717
 Db 61 CTGTGAACTGCGAATGCTCAATTAAGTATAGTTATTTGATGCTACCTTGCTAC 120

Qy 718 ATGCATAACTGTGCTAAATTTCTAGA 741
 Db 121 ATGCATAACTGTGCTAAATTTCTAGA 144

RESULT 9
 AAV31379
 ID AAV31379 standard; DNA; 5373 BP.
 XX
 AC AAV31379;
 XX
 XX 07-SEP-1998 (first entry)
 DT
 DE Arabidopsis thaliana rRNA gene intergenic region.
 XX
 KW Arabidopsis thaliana; rRNA gene; ribosomal DNA; intergenic region;
 KW DNA-construct; plant; multiple Sali repeat; stability; copy number;
 KW transgene; antibody; insecticidal protein; Bt toxin; ds.
 XX
 OS Arabidopsis thaliana.
 XX

Key Location/Qualifiers
 FT misc_feature 1..485
 FT /tag= a
 FT /note= "25S rDNA 3'-end"
 FT 486..5211
 FT misc_feature /tag= b
 FT /note= "intergenic region"
 FT 1263..1557
 FT misc_feature /tag= c
 FT /note= "Sali box 1"
 FT 1883..2177
 FT misc_feature /tag= d
 FT /note= "Sali box 2"
 FT 2503..3003
 FT misc_feature /tag= e
 FT /note= "Sali box 3"
 FT 5212..5373
 FT misc_feature /tag= f
 FT /note= "18S rDNA 5'-end"
 XX
 XX WO9813505-A1.
 XX PN
 XX 02-APR-1998.
 XX PD
 XX 23-SEP-1997; 97WO-EP005217.
 XX PF
 XX 24-SEP-1996; 96AT-00001695.
 XX PR
 XX (PLBZ) PLANT GENETIC SYSTEMS NV.
 XX PA
 XX Bachmair A, Schweizer D;
 XX PI

XX DR WPI; 1998-286413/25.
XX PT DNA construct containing plant intergenic ribosomal DNA fragment -
XX PT containing multiple Sali repeats; increases stability and copy number of
XX PT a transgene(s) in plants.
XX PS Claim 7; Page 23-28; 48pp; English.
XX CC A linked construct has been developed which comprises the following operably
XX CC linked DNA fragments: (a) a ribosomal DNA sequence, preferably derived
XX CC from a plant; (b) an expressible (especially plant-expressible) promoter
XX CC region; (c) a heterologous coding region; and (d) a transcription
XX CC termination and polyadenylation region which preferably is active in
XX CC plant cells. The present sequence represents the DNA sequence of the
XX CC intergenic region of rRNA gene repeats of Arabidopsis thaliana, fragments
XX CC of which can be used in a DNA construct of the invention. Transformed
XX CC plant cells and transgenic plants comprising the DNA constructs are used
XX CC to produce a desired protein at a high yield, e.g. antibodies,
XX CC insecticidal proteins (e.g. a Bt toxin), a protein useful in the food
XX CC industry. Alternatively the constructs can be used to produce an
XX CC antisense RNA or ribozyme. The use of intergenic ribosomal DNA enhances
XX CC stability and the copy number or expression of transgenes in a plant
XX CC
SQ Sequence 5373 BP; 1431 A; 1134 C; 1514 G; 1294 T; 0 U; 0 Other;

Query Match 18.2%; Score 134.6; DB 2; Length 5373;
Best Local Similarity 91.1%; Pred. No. 4.8e-33;
Matches 154; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 573 GATAGTTACCTGGTGGATCCTGCCAGTAGTCATATGCTTGTCTCAAGATTAAAGCCATGC 632
DB 5206 GAATGCTACCTGGTGGATCCTGCCAGTAGTCATATGCTTGTCTCAAGATTAAAGCCATGC 5265
QY 633 ATGTCTAAGTATAACAAATTCACTGTGAACCTGCGAATGGCTCAATTAATCAGTTAT 692
DB 5266 ATGTGTAAGTATGAACGAATTCACTGTGAACCTGCGAATGGCTCAATTAATCAGTTAT 5325
QY 693 AGTTTATTGTTGATGCTTGTCTCAAGATTAAAGCCATGC 741
DB 5326 AGTTTATTGTTGATGCTTGTCTCAAGATTAAAGCCATGC 5373

RESULT 10
AAAF22281
ID AAF22281 standard; DNA; 59590 BP.
XX AC AAF22281;
XX AC AAF22281;
XX DT 20-MAR-2001 (first entry)
XX DE BAC containing repeats from centromeres 1-4 #4.
XX KW Centromere; microsome; vector; ds.
XX OS Arabidopsis thaliana.
XX XX WO200055325-A2.
XX PD 21-SEP-2000.
XX PF 17-MAR-2000; 2000WO-US0007392.
XX PR 18-MAR-1999; 99US-0125219P.
XX PR 01-APR-1999; 99US-0127409P.
XX PR 18-MAY-1999; 99US-0134770P.
XX PR 13-SEP-1999; 99US-0153584P.
XX PR 17-SEP-1999; 99US-0154603P.
XX PR 16-DEC-1999; 99US-0172493P.
XX XX (UYCH-) UNIV CHICAGO.
XX PA Preuss D, Copenhagen G, Keith K;
XX PI

XX DR WPI; 2000-587529/55.
XX PT Recombinant DNA construct comprising a plant centromere, useful for
XX PT producing stably inherited microsome which can serve as vectors for the
XX PT construction of transgenic plant and animal cells.
XX PS Claim 102; Page 351-364; 1449pp; English.
XX CC The present invention relates to a recombinant DNA construct of a plant
XX CC (Arabidopsis thaliana) centromere. The constructs are useful for
XX CC producing stably inherited microsome which can serve as vectors for the
XX CC construction of transgenic plant and animal cells expressing selected
XX CC proteins such as hormones, enzymes, interleukins, clotting factors,
XX CC cytokines, antibodies, and growth factors
XX CC
SQ Sequence 59590 BP; 17614 A; 12031 C; 13575 G; 16118 T; 0 U; 252 Other;
Query Match 18.2%; Score 134.6; DB 3; Length 59590;
Best Local Similarity 91.1%; Pred. No. 1.8e-32;
Matches 154; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 573 GATAGTTACCTGGTGGATCCTGCCAGTAGTCATATGCTTGTCTCAAGATTAAAGCCATGC 632
DB 42736 GAATGCTACCTGGTGGATCCTGCCAGTAGTCATATGCTTGTCTCAAGATTAAAGCCATGC 42795
QY 633 ATGTCTAAGTATAACAAATTCACTGTGAACCTGCGAATGGCTCAATTAATCAGTTAT 692
DB 42796 ATGTGTAAGTATGAACGAATTCACTGTGAACCTGCGAATGGCTCAATTAATCAGTTAT 42855
QY 693 AGTTTATTGTTGATGCTTGTCTCAAGATTAAAGCCATGC 741
DB 42856 AGTTTATTGTTGATGCTTGTCTCAAGATTAAAGCCATGC 42903

RESULT 11
ADFS4865
ID ADFS4865 standard; DNA; 3172 BP.
XX AC ADFS4865;
XX AC ADFS4865;
XX DT 12-FEB-2004 (first entry)
XX DE Ribosomal DNA spacer region utilising rice DNA, SEQ ID No 1.
XX KW spacer region; ribosomal DNA; rDNA; promoter; expression; plant; rice;
XX KW ds.
XX OS Oryza sativa.
XX XX JP2003135067-A.
XX PD 13-MAY-2003.
XX PF 30-OCT-2001; 2001JP-00332861.
XX PR 30-OCT-2001; 2001JP-00332861.
XX PA (MITA) MITSUI CHEM INC.
XX XX WPI; 2003-771330/73.
XX XX Utilizing DNA containing all nucleotide sequences of spacer region of
XX PT rDNA and whose G and C content exceeds 50% as enhancer which activates
XX PT promoter of foreign cell.
XX PS Example 2; SEQ ID NO 1; 10pp; Japanese.
XX CC The invention relates to the novel method for utilising DNA containing
XX CC all the nucleotides sequences of a spacer region of ribosomal DNA (rDNA).
XX CC The invention further comprises a nucleotide sequence containing a
XX CC repeated rDNA spacer region sequence, or nucleotide sequence originating
XX CC from the sequence and the total amount of G+C content exceeds 50%. The

CC spacer region containing DNA is useful as an enhancer which activates the
 CC promoter of foreign cell. The invention also provides a method for
 CC increasing expression in one or more foreign cell(s) in one or more
 CC organ(s) of plant, by increasing activity of the promoter of one or more
 CC foreign gene involving the use of the spacer region containing DNA; a
 CC chimeric gene containing the spacer region containing DNA and a gene
 CC promoter, coding sequence or non-coding sequence and terminator sequence;
 CC a transformed plant containing the chimeric gene; and a cell in which
 CC expression of a foreign gene is increased by the novel methods of the
 CC invention. This polynucleotide represents a rice DNA sequence used in the
 CC novel spacer region DNA utilising method of the invention.

CC SQ Sequence 3172 BP; 591 A; 1047 C; 1041 G; 493 T; 0 U; 0 Other;

Query Match 17.8%; Score 132.2; DB 10; Length 3172;

Best Local Similarity 91.5%; Pred. No. 2.3e-32;

Matches 151; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Qy 577 GTTACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCAAGATTAAAGCCATGCTGT 636

Db 2623 GCTACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCAAGATTAAAGCCATGCTGT 2682

Qy 637 CTAAGTATAACAATAATTCATATCTGGAACCTGCGAATGGCTCATTTAAATCAGTTTATAGTT 696

Db 2683 GCAAGTAATGAATAATTCGAATCTGGAACCTGCGAATGGCTCATTTAAATCAGTTTATAGTT 2742

Qy 697 TATTTGATGGTACCTTGCTACATGGATAACTGTGGTAAATCTTCTAGA 741

Db 2743 TGTTTGATGGTA-CGTGCTACTCGGATAACCGTAGTAATCTTCTAGA 2786

RESULT 12

ADRO1486/c

ID ADRO1486 standard; DNA; 703 BP.

XX AC ADRO1486;

DT 23-SEP-2004 (first entry)

DE A. gossypii genomic DNA PAG1070RP.

XX Filamentous funghi; ds; forensic identification; gene characterisation;
 XX intergenomic comparison; chromosome mapping.

XX Erethothecium gossypii.

XX US6239264-B1.

XX PD 29-MAY-2001.

XX PF 24-DEC-1997; 97US-00998416.

XX PR 31-DEC-1996; 97CH-00000016.

XX PA (SYNG-) SYNGENTA PARTICIPATIONS AG.

XX PI Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;

XX PI Knechtle P, Reibischung C;

XX DR WPI; 1998-388120/33.

XX New gene for adenylate cyclase from *Ashbya gossypii* - useful for
 PT generating recombinant microorganisms with alteration in gene of camp-
 PT dependent signalling pathway for increasing production of fine chemicals.

XX Example 3; SEQ ID NO 178; 632pp; English.

XX The invention relates to isolated DNA molecules comprising isolated
 CC genomic DNA sequences from the filamentous funghi *Ashbya gossypii*, the
 CC sequences comprising ADRO1309, ADRO1366, ADRO1367, ADRO1388, ADRO1428,
 CC ADRO1466, ADRO1629, ADRO1637, ADRO2057, ADRO2345 and ADRO2369, chosen
 CC from 1047 disclosed genomic sequences. Also included is a cloning vector
 CC comprising a nucleotide sequence chosen from the above sequences. The
 CC novel *Ashbya gossypii* genomic sequences are useful for forensic
 CC identification, gene characterisation, for studying gene organisation by
 CC intergenomic comparison (with *Saccharomyces cerevisiae*), identifying

CC novel *Ashbya gossypii* genomic sequences are useful for forensic
 CC identification, gene characterisation, for studying gene organisation by
 CC intergenomic comparison (with *Saccharomyces cerevisiae*), identifying
 CC biosynthetic genes for selectable markers, to isolate
 CC promoters/terminators/centromeres, chromosome mapping, and in identifying
 CC sequences unique to *Ashbya gossypii* for species identification. The
 CC present sequence is an *A. gossypii* novel genomic sequence of the
 CC invention.

CC SQ Sequence 703 BP; 210 A; 165 C; 129 G; 197 T; 0 U; 2 Other;

Query Match 17.8%; Score 131.6; DB 2; Length 703;

Best Local Similarity 93.5%; Pred. No. 1.6e-32;

Matches 159; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

Qy 573 GATAGTTACCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCAAGATTAAAGCCATGC 632

Db 686 GATAGTTATCTGGTTGATCCTGCCAGTAGTCATATGCTTGCTCAAGATTAAAGCCATGC 627

Qy 633 ATGCTTAAGTATAACAATAATTCATATCTGGAACCTGCGAATGGCTCATTTAAATCAGTTAT 692

Db 626 ATGCTTAAGTATAAGC-AAITTTATACAGTGAACCTGCGAATGGCTCATTTAAATCAGTTAT 568

Qy 693 AGTTTATTTGATGCTACC-TTGCTACATGGATAACTGTGGTAAATCTTCTAGA 741

Db 567 CGTTTATTTGATAGTTCCCTTTACTACATGGATATCTGTGGTAAATCTTCTAGA 518

RESULT 13

ADRO2122

ID ADRO2122 standard; DNA; 706 BP.

XX AC ADRO2122;

DT 23-SEP-2004 (first entry)

DE A. gossypii genomic DNA PAG1518UP.

XX Filamentous funghi; ds; forensic identification; gene characterisation;
 XX intergenomic comparison; chromosome mapping.

XX Erethothecium gossypii.

XX US6239264-B1.

XX PD 29-MAY-2001.

XX PF 24-DEC-1997; 97US-00998416.

XX PR 31-DEC-1996; 97CH-00000016.

XX PA (SYNG-) SYNGENTA PARTICIPATIONS AG.

XX PI Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;

XX PI Knechtle P, Reibischung C;

XX DR WPI; 1998-388120/33.

XX New gene for adenylate cyclase from *Ashbya gossypii* - useful for
 PT generating recombinant microorganisms with alteration in gene of camp-
 PT dependent signalling pathway for increasing production of fine chemicals.

XX Example 3; SEQ ID NO 814; 632pp; English.

XX The invention relates to isolated DNA molecules comprising isolated
 CC genomic DNA sequences from the filamentous funghi *Ashbya gossypii*, the
 CC sequences comprising ADRO1309, ADRO1366, ADRO1367, ADRO1388, ADRO1428,
 CC ADRO1466, ADRO1629, ADRO1637, ADRO2057, ADRO2345 and ADRO2369, chosen
 CC from 1047 disclosed genomic sequences. Also included is a cloning vector
 CC comprising a nucleotide sequence chosen from the above sequences. The
 CC novel *Ashbya gossypii* genomic sequences are useful for forensic
 CC identification, gene characterisation, for studying gene organisation by
 CC intergenomic comparison (with *Saccharomyces cerevisiae*), identifying

SQ Sequence 712 BP; 184 A; 145 C; 170 G; 213 T; 0 U; 0 Other;

Query Match 17.5%; Score 130; DB 2; Length 712;
Best Local Similarity 92.9%; Pred. No. 5.4e-32;
Matches 158; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

Qy 573 GATAGTTACCTGGTTGATCCTGCCAGTAGTCATATGTTGCTCAAGATTAAAGCCATGC 632
Db 498 GATAGTTATCTGGTTGATCCTGCCAGTAATCATATGCTTGTCTCAAGATTAAAGCCATGC 557

Qy 633 ATGCTAAGTATAAACAATAATTCATACTGTGAACTGGGAATGGCTCATTAATCAGTTAT 692
Db 558 ATGCTAAGTATAAGC-AAATTATACAGTGAACCTGGGAATGGCTCATTAATCAGTTAT 616

Qy 693 AGTTTATTGATGTACC-TTGCTACATGGATACTGTGGTAATCTAGA 741
Db 617 CGTTTATTGATAGTTCTCTTACTACATGGATATCTGTGGTAATCTAGA 666

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Job time : 453.315 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
9974.329 Million cell updates/sec

Title: US-09-830-691A-1
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	1223	6	BD237786
2	1215	99.3	2552	8	AF004672
3	147.6	12.1	350	6	BD237787
4	115	9.4	336	8	CRU31912
5	113.8	9.3	110000	8	CH382128_05
6	107.8	8.8	688	6	AR382552
7	107.8	8.8	1048	8	YSRQPL41
8	107.8	8.8	2086	6	AR065319
9	107.8	8.8	2086	6	E11620
10	107.8	8.8	2086	6	AR382551
11	107.8	8.8	2086	8	YSAREL41
12	107.8	8.5	444	8	RIC340
13	103.4	8.5	676	8	AK058924
14	103.4	8.5	2173	8	AK069083
15	103.4	8.5	1611	8	AB021315
16	102.8	8.4	1611	8	AB021315
17	101.4	8.3	110000	8	CH380953_05
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19	101	8.3	480	8	CNS018R9

20	101	8.3	480	8	CNS01A80	AL112624 Botrytis
21	101	8.3	480	8	CNS01AXH	AL113517 Botrytis
22	101	8.3	516	8	CNS01AGD	AL112901 Botrytis
23	101	8.3	518	8	CNS0190P	AL111040 Botrytis
24	101	8.3	540	8	CNS019IQ	AL111690 Botrytis
25	101	8.3	540	8	CNS01A0U	AL112342 Botrytis
26	101	8.3	540	8	CNS01C7X	AL115189 Botrytis
27	101	8.3	540	8	CNS01CSO	AL115936 Botrytis
28	101	8.3	540	8	CNS01D75	AL116457 Botrytis
29	101	8.3	540	8	CNS01DEP	AL116729 Botrytis
30	101	8.3	540	8	CNS01DN9	AL117037 Botrytis
31	101	8.3	636	8	CNS01D5A	AL116390 Botrytis
32	101	8.3	681	5	EC055187	BC055187 Danio rer
33	101	8.3	840	8	CNS01BEI	AL114130 Botrytis
34	100.6	8.2	1828	8	YSKFL41	D10580 Kluyveromyc
35	99.8	8.2	321	5	AJ605265	AJ605265 Platicht
36	99	8.1	12855	8	SPAC15E1	AL109770 S.pombe c
37	98.2	8.0	412	5	AF401592	AF401592 Ictalurus
38	98.2	8.0	1333	6	AX073124	AX073124 Sequence
39	98.2	8.0	1975	8	YSCSCL41A	D10578 Saccharomyc
40	98.2	8.0	2523	8	SCYNL162W	271438 S.cerevisia
41	98.2	8.0	36813	8	SCORFSC14	X92517 S.cerevisia
42	97.8	8.0	306906	8	AE016900	AE016900 Ermothec
43	96.6	7.9	1282	6	AX073018	AX073018 Sequence
44	96.6	7.9	1823	8	YSCSCL41B	D10579 Saccharomyc
45	96.6	7.9	30350	8	YSCH9315	U10398 Saccharomyc

ALIGNMENTS

RESULT 1
LOCUS BD237786 1223 bp DNA linear PAT 17-JUL-2003
DEFINITION Phaffiarhodozyma transforming vectors and transforming method
thereof.
ACCESSION BD237786
VERSION BD237786.1 GI:33047556
KEYWORDS JP 2002528124-A/1.
SOURCE Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)
ORGANISM Xanthophyllomyces dendrorhous
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
Cystofilobasidiaceae; Xanthophyllomyces.
REFERENCE 1 (bases 1 to 1223)
AUTHORS Choi,E.S., Rhee,S.K., Sohn,J.H., Park,S.D., Lee,Y.H., Lee,S.J.,
Jang,J.K., Choi,S.K. and Son,Y.R.
TITLE Phaffiarhodozyma transforming vectors and transforming method
JOURNAL Patent: JP 2002528124-A 1 03-SEP-2002;
KOREA INSTITUTE OF SCIENCE AND TECHNOLOGY, HAITAI CONFECTIONERY CO
LTD
COMMENT OS Phaffia rhodozyma
PN JP 2002528124-A/1
PD 03-SEP-2002
PF 29-MAY-1999 JP 2000579759
PR 31-OCT-1998 KR 1998/46547
PI EUI SUNG CHOI,SANG KI RHEE,JUNG HOON SOHN,SOO DONG PARK,YOON
PI HYOUNG LEE
PI SEUNG JAE LEE, JAE KWEON JANG, SEOK KEUN CHOI, YOUNG ROK SON PC
C12N15/09,C12N1/19//C12N1/19,C12R1:645),C12N15/00 CC
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thereof
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/mol_type='genomic DNA'
/db_xref='taxon:5421'

Query Match 100.0%; Score 1223; DB 6; Length 1223;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1223; Conservative 0;

QY 1 ATGTCACAGCTTCCCAAGACTCGAGTGTAGCAATTTCAACAACCTCTCCAGACGA 60
DB 1 ATGTCACAGCTTCCCAAGACTCGAGTGTAGCAATTTCAACAACCTCTCCAGACGA 60
QY 61 CAAATATTCAGTGCATCGAAGAGTTTGTGGATTAACCGGACAGTTTCAAGGGAAGAG 120
DB 61 CAAATATTCAGTGCATCGAAGAGTTTGTGGATTAACCGGACAGTTTCAAGGGAAGAG 120
QY 121 TCGATGACAGATTTGGAAGACTTAGCGGTCAGGAACTTGGGATCACTGCGCGAGG 180
DB 121 TCGATGACAGATTTGGAAGACTTAGCGGTCAGGAACTTGGGATCACTGCGCGAGG 180
QY 181 ACTCATCAGAAAGTCCGGATTTGTTGATCATATGAGTGGATCAAGCAAACTGGAGAT 240
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QY 241 ATGCTCGCCTTGAAGGATCTCCGCTCGGATTCGAGATCCGAAAGTTGTACGTAT 300
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QY 361 CTTGCAAGACACACGTAAGTCTCTCCATCTTTCATGCGATTTGTCAAC 420
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QY 721 TTTCACAGAGGCTTACACCAAGAGTCTGCTTCTGATTTGGCGGTATTTTGT 780
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QY 841 CTCCTCAACACAGAGTCTCGCTGAGTCTGCTTCTCTTCTTCCACCAAACTTCACTA 900
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QY 1081 CTTTTTGGTTCGGATGTTGTTTCTATCGTGTGTTTCTTCTTTCTTTGGATGCAATATC 1140
DB 1081 CTTTTTGGTTCGGATGTTGTTTCTATCGTGTGTTTCTTCTTTCTTTGGATGCAATATC 1140
QY 1141 ATTATCGTGTGAGTGTTCCTCTGCTGCTGCTTCTTCTTCTCTGTAATGCTGTTCT 1200
DB 1141 ATTATCGTGTGAGTGTTCCTCTGCTGCTGCTTCTTCTTCTCTGTAATGCTGTTCT 1200
QY 1201 CAGGAGCCGCCATCTCTTTCTAA 1223
DB 1201 CAGGAGCCGCCATCTCTTTCTAA 1223

RESULT 2

AF004672 2552 bp DNA linear PLN 18-MAR-1999
LOCUS Xanthophyllomyces dendrorhous ribosomal protein L41 (L41) gene,
DEFINITION complete cds.
ACCESSION AF004672 GI:3128242
VERSION AF004672.1
KEYWORDS Phaffia rhodozyma
SOURCE Phaffia rhodozyma
ORGANISM Phaffia rhodozyma
Phaffia rhodozyma
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
mitosporic Cystofilobasidiales; Phaffia.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Kim, I.G., Nam, S.K., Sohn, J.H., Rhee, S.K., AN, G.H., Lee, S.H. and
Choi, E.S.
TITLE Cloning of the ribosomal protein L41 gene of Phaffia rhodozyma and
its use as a drug resistance marker for transformation
JOURNAL Appl. Environ. Microbiol. 64 (5), 1947-1949 (1998)
MEDLINE 98247333
PUBMED 9572978
REFERENCE 2 (bases 1 to 2552)
AUTHORS Kim, I.G., Choi, E.-S. and Lee, S.-K.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-1997) Applied Microbiology Research Division,
Korea Research Institute of Bioscience and Biotechnology, Taejeon,
Korea

FEATURES

source Location/Qualifiers
1. 2552
/organism="Phaffia rhodozyma"
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/db_xref="taxon:264483"
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Phaffia rhodozyma"
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Query Match 99.3%; Score 1215; DB 8; Length 2552;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGTCACAGTTCACCAAGACTCGAGTGTAGCAATTTCAACAACCTCTCCAGACGA 60

Db 845 ATGGTCAACAGTTCCTCCAAAGACTCGACGTGAGTTATAGCAATTTCAACAACTCTCAGACGA 904
Qy 61 CAATATATTCAGTGCATCGAAAGAGTTTGTGGATAAAGCGACAGTTTCAAGGCGAAAGAG 120
Db 905 CAATATATTCAGTGCATCGAAAGAGTTTGTGGATAAAGCGACAGTTTCAAGGCGAAAGAG 964
Qy 121 TCGATGGACAGATTGGGAAGACTTAGCCGGTCAAGGAACCTTGGGGATCACTGCGGAGG 180
Db 965 TCGATGGACAGATTGGGAAGACTTAGCCGGTCAAGGAACCTTGGGGATCACTGCGGAGG 1024
Qy 181 ACTCATCAGAAGAGTCCGGGATTTGTTGATCATAGTGGGATCAAGCAAACTCGAGAT 240
Db 1025 ACTCATCAGAAGAGTCCGGGATTTGTTGATCATAGTGGGATCAAGCAAACTCGAGAT 1084
Qy 241 ATGGCTCGCTTGGGAAGGGAATCTCCGGCCCTGGGATTCGAGGATCCGAAGTTGTACGTAT 300
Db 1085 ATGGCTCGCTTGGGAAGGGAATCTCCGGCCCTGGGATTCGAGGATCCGAAGTTGTACGTAT 1144
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Db 1145 GGAAGCTTACACGGCTTGGATTTATATCTTTTCATAGGAACCTACTGCAAGGGTAAAG 1204
Qy 361 CTTCAGAGACACAGTGAAGTCTTATCTCTCCACTCTTTCATGCGATATTTGTCAAC 420
Db 1205 CTTCAGAGACACAGTGAAGTCTTATCTCTCCACTCTTTCATGCGATATTTGTCAAC 1264
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Db 1325 TGTATTTAGCCCTCACAAGGTACATATACATCTCCACCCACCCCTGCGCCAACTCTTT 1384
Qy 541 CAGTTTCACTTGTCTCGGTTTTCACATTCCTCGATGACCTCTGTATGTTCTTTGGGA 600
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Db 1445 ACCTTTGTTTCTGTTCTGTAGGTGACCCAGTACAGGAAGGAAGGACTCCATCTTCGC 1504
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Db 1505 CCAGGGAAGCGACGATACGACCGAAAGCAGTCCGGTTACGAGGTGAGCAACCAAGCCCGT 1564
Qy 721 TTTCACAGAGGCTAAGACCAACAGAGGTCGTCTTCGATTCGGGTATTTTGT 780
Db 1565 TTTCACAGAGGCTAAGACCAACAGAGGTCGTCTTCGATTCGGGTATTTTGT 1624
Qy 781 TATTTTGAATTTCTTTTGTGATGATGATTTTGTGATGATGATGATGATGATGATGATGAT 840
Db 1625 TATTTTGAATTTCTTTTGTGATGATGATTTTGTGATGATGATGATGATGATGATGATGAT 1684
Qy 841 CTCTTCAACAGAGTGTCCGTCTGCGAGTTCGTCTCTTCTTCCAAACCAAACTTCAACTA 900
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Db 1745 CAGACATCATAAACAGACATCTTACTTCGGTGTCTCTCTTTTTCGGCAGAGTACAAG 1804
Qy 961 ATGCAGATGACCTTCAAGCGATGCAAGCATTCCAGCTTGGAGGAGCAAGAGACCAAG 1020
Db 1805 ATGCAGATGACCTTCAAGCGATGCAAGCATTCCAGCTTGGAGGAGCAAGAGACCAAG 1864
Qy 1021 GGTTTCGTTTGTCCATATATCTCTGGTTCACCTTATGTTCTTAAAGTACTTGT 1080
Db 1865 GGTTTCGTTTGTCCATATATCTCTGGTTCACCTTATGTTCTTAAAGTACTTGT 1924
Qy 1081 CTTTTCGTTTGTTCGATGTTGTTTCTATCGGTTGTTTCTTTTCTTTTGTGATGATTC 1140

Db 1925 CTTTTCGTTTGTTCGATGTTGTTTCTATCGGTGGTGTTCCTTTCTTTCTTTGGAGCATATC 1984
Qy 1141 ATTTATCGTGTGACATGTTTTCCTCTGCTGCTGCTTCTTCTCTCTCTGCTGCTGCTTCT 1200
Db 1985 ATTTATCGTGTGACATGTTTTCCTCTGCTGCTTCTCTCTCTCTCTGCTGCTGCTTCT 2044
Qy 1201 CAGGAGCCGCATCTCTTTCTAA 1223
Db 2045 CAGGAGCCGCATCTCTTTCTAA 2067
RESULT 3
BD237787
LOCUS Phaffiarhodozyma 350 bp DNA linear PAT 17-JUL-2003
DEFINITION Phaffiarhodozyma transforming vectors and transforming method
thereof.
ACCESSION BD237787
VERSION BD237787.1 GI:33047557
KEYWORDS JP 2002528124-A/2.
SOURCE Xanthophyllomyces dendrorhous
ORGANISM Xanthophyllomyces dendrorhous
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
Cystofilobasidiaceae; Xanthophyllomyces.
REFERENCE 1 (bases 1 to 350)
AUTHORS Choi, E.S., Rhee, S.K., Sohn, J.H., Park, S.D., Lee, Y.H., Lee, S.J.,
Jang, J.K., Choi, S.K. and Son, Y.R.
TITLE Phaffiarhodozyma transforming vectors and transforming method
JOURNAL Patent: JP 2002528124-A 2 03-SEP-2002;
KOREA INSTITUTE OF SCIENCE AND TECHNOLOGY, HAITAI CONFECTIONERY CO
LTD
COMMENT OS Phaffia rhodozyma
PN JP 2002528124-A/2
PD 03-SEP-2002
PF 29-MAY-1999 JP 2000579759
PR 31-OCT-1998 KR 1998/46547
PI EUI SUNG CHOI, SANG KI RHEE, JUNG HOON SOHN, SOO DONG PARK, YOON
PI HYOUNG LEE,
PI SEUNG JAE LEE, JAE KWEON JANG, SEOK KEUN CHOI, YOUNG ROK SON PC
C12N15/09, C12N1/19/(C12N1/19, C12R1:645), C12N15/00 CC
Phaffiarhodozyma transforming vectors and transforming method CC
thereof
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
source 1..350
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ORIGIN
Query Match 12.1%; Score 147.6; DB 6; Length 350;
Best Local Similarity 97.4%; Pred. No. 1.6e-29;
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 616 TCTGTAGTGTCACCCAGTACCAAGGAAGGAAAGGACTCCATCTTCGCCAGGAAAGCGACG 675
Db 95 TCACAGGTGACCCAGTACCAAGGAAGGAAAGGACTCCATCTTCGCCAGGAAAGCGACG 154
Qy 676 ATACGACCGAAAGCAGTCCGGTTACGGAGTTCAGACCAAGCCGCTTTTCCACGAAGAGGC 735
Db 155 ATACGACCGAAAGCAGTCCGGTTACGGAGGTCAGACCAAGCCGCTTTTCCACGAAGAGGC 214
Qy 736 TAGACCCACCAAGAGTTCGCTTCGATTGGCG 769
Db 215 TAAGACCCACCAAGAGTTCGCTTCGATTGGAG 248
RESULT 4
CRU31912
LOCUS Chlamydomonas reinhardtii ribosomal protein L41 (RPL41) mRNA,
DEFINITION complete cds.

ACCESSION U1912
VERSION U1912.1 GI:974301
KEYWORDS
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 336)
AUTHORS Stevens,D.R., Actea,A., Franzen,L.-G. and Purton,S.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-1995) Saul Purton, Biology, University College
London, wer Street, London WC1E 6BT, UK
FEATURES
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/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="137C (cw15)"
/db_xref="taxon:3055"
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QSGYGGQTKPVFHKAKTKTKVLRMQCEKQTCMKGLKRCRKHFEIGGDKKGN"

ORIGIN

Query Match 9.4%; Score 115; DB 8; Length 336;
Best Local Similarity 83.9%; Pred. No. 1.7e-20;
Matches 130; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 612 TGTCTCTAGTGTACCCAGTACAGAGGAAAGGACTCCATCTTCGCCAGGAAAGC 671
DB 67 TGATGATGAAGTACACCCAGTACAGACTGCGAGGCTCCCTCTACCGCAGGCGAAGC 126
QY 672 GACGATACGACCGAAGCAGTCGGTTACGAGGTTCAGACCAAGCCGCTTTCCACAAGA 731
DB 127 GCGCTACGACCGCAAGCAGTCGGTTACGAGGTTCAGACCAAGCCGCTTTCCACAAGA 186
QY 732 AGGCTAAGACCAAGCAGTTCGCTTCGATTG 766
DB 187 AGGCCAAGACCAAGCAGTTCGCTTCGATTG 221

RESULT 5

CR382128_05
WPCOMMENT
Sequence split into 31 fragments LOCUS CR382128 Accession CR382128

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CR382128_02	200001	310000
CR382128_03	300001	410000
CR382128_04	400001	510000
CR382128_05	500001	610000
CR382128_06	600001	710000
CR382128_07	700001	810000
CR382128_08	800001	910000
CR382128_09	900001	1010000
CR382128_10	1000001	1110000
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CR382128_16	1600001	1710000
CR382128_17	1700001	1810000

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CR382128_29 2900001 3010000
CR382128_30 3000001 3066374
Continuation (6 of 31) of CR382128 from base 500001 (CR382128 Yarrowia lipolytica chromo

Query Match 9.3%; Score 113.8; DB 8; Length 110000;
Best Local Similarity 85.2%; Pred. No. 5.3e-20;
Matches 127; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGAAAGCGCATACG 680
DB 61442 AGGTGACCCAGTACAAAGGCGGTAAAGCTTCTCTGACGTCAGGGTAAGCGCATACG 61501
QY 681 ACCGAAAGCAGTCCGTTACGAGGTACAGCCAGCCGCTTTCCACAAGAGGCTTAAGA 740
DB 61502 ACCGAAAGCAGTCCGTTACGAGGTACAGCCAGCAGATTTTCCACAAGAGGCGCAAGA 61561
QY 741 CCACCAAGAGGTGCTCTTCGATTTCGCGG 769
DB 61562 CCACCAAGAGGTGCTTCGCGACTCGAG 61590

RESULT 6

AR382552
LOCUS AR382552 688 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6610514.
ACCESSION AR382552
VERSION AR382552.1 GI:40091283
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 688)
AUTHORS Kondo, K. and Miura, Y.
TITLE Yeast vector and method of producing proteins using the same
JOURNAL Patent: US 6610514-A 38 26-AUG-2003;
FEATURES
source Location/Qualifiers
1..688
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 8.8%; Score 107.8; DB 6; Length 688;
Best Local Similarity 79.9%; Pred. No. 1.8e-18;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGAAAGCGCATACG 680
DB 438 AGGTGACCCAGTACAAAGGCTGTTAAAGCTTCCCTTTGCGGAGGTAAAGCTGTTATG 497
QY 681 ACCGAAAGCAGTCCGTTACGAGGTACAGCCAGCCGCTTTCCACAAGAGGCTTAAGA 740
DB 498 ACCGTAAGCAATCCGTTACGAGGTCAACCAAGCAGATTTTCCACAAGAGGCTTAAGA 557
QY 741 CCACCAAGAGGTGCTCTTCGATTTCGCGGTATTTTGT 779
DB 558 CCACCAAGAGGTGTTTTCGTTGAGTGTGTGTCT 596

RESULT 7

YSRPGL41
LOCUS YSRPGL41 1048 bp DNA linear PLN 06-NOV-2001
DEFINITION Pichia guilliermondii PGL41 gene for ribosomal protein L41, partial

ACCESSION D10153
 VERSION D10153.1 GI:218561
 KEYWORDS
 SOURCE
 ORGANISM
 Pichia guilliermondii
 Pichia guilliermondii
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Pichia.
 REFERENCE
 1 (bases 1 to 1048)
 Kawai, S.
 Unpublished
 These data kindly submitted in computer readable form by: Shinya
 Kawai
 Dept. Agricultural Chemistry
 The University of Tokyo
 Bunkyo-ku, Tokyo 113
 Japan
 Phone: 03-3812-2111 x3087
 Fax: 03-3812-9246
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 Best Local Similarity 70.0%; Pred. No. 1.8e-18;
 Matches 145; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 Qy 561 TTCACATTCCTGATGACCTCTTGTATGTTCTTTCGAAAGCTTCTGTTCTGTTCTGT 620
 Db 749 TTCCAAAGACCAAGAGAACTTCTGCAAGGTAAGACTGCGTAAGCACACCAACACA 808
 Qy 621 AGGTGACCCAGTACAGAGGAAAGACTCCATCTTCGCCAGGAAAGCGAGTACG 680
 Db 809 AGGTGACCCATACAGAGGTAAGGCTCTTTGTTGCCAGGGTAAGAGATATG 868
 Qy 681 ACCGAAAGCAGTCGGTTACGAGGTACAGCAAGCCGTTTCCACAAGAGCTAAGA 740
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 Qy 741 CCACCAAGAGGTGCTCTTCGATTGG 767
 Db 929 CTACCAAGAGGTGTTGTGATTGG 955
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 AR065319
 LOCUS
 DEFINITION Sequence 5 from patent US 5849524.
 ACCESSION AR065319
 VERSION AR065319.1 GI:5995535
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 2086)
 Kondo, K., Kajiwara, S. and Misawa, N.
 Transformation systems for the yeast candida utilis and the
 expression of heterologous genes therewith
 Patent: US 5849524-A 5 15-DEC-1998;
 Location/Qualifiers
 cds.
 D10153
 VERSION D10153.1 GI:218561
 KEYWORDS
 SOURCE
 ORGANISM
 Pichia guilliermondii
 Pichia guilliermondii
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Pichia.
 REFERENCE
 1 (bases 1 to 1048)
 Kawai, S.
 Unpublished
 These data kindly submitted in computer readable form by: Shinya
 Kawai
 Dept. Agricultural Chemistry
 The University of Tokyo
 Bunkyo-ku, Tokyo 113
 Japan
 Phone: 03-3812-2111 x3087
 Fax: 03-3812-9246
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 Best Local Similarity 70.0%; Pred. No. 1.8e-18;
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 Qy 561 TTCACATTCCTGATGACCTCTTGTATGTTCTTTCGAAAGCTTCTGTTCTGTTCTGT 620
 Db 749 TTCCAAAGACCAAGAGAACTTCTGCAAGGTAAGACTGCGTAAGCACACCAACACA 808
 Qy 621 AGGTGACCCAGTACAGAGGAAAGACTCCATCTTCGCCAGGAAAGCGAGTACG 680
 Db 809 AGGTGACCCATACAGAGGTAAGGCTCTTTGTTGCCAGGGTAAGAGATATG 868
 Qy 681 ACCGAAAGCAGTCGGTTACGAGGTACAGCAAGCCGTTTCCACAAGAGCTAAGA 740
 Db 869 ACCGTAAGCAATCGGTTTCGGTGTCAACCAAGCCGTTTCCACAAGAGCCCAAGA 928
 Qy 741 CCACCAAGAGGTGCTCTTCGATTGG 767
 Db 929 CTACCAAGAGGTGTTGTGATTGG 955
 RESULT 8

YSRQLAP
 LOCUS
 DEFINITION Pichia sp. ribosomal protein L41 gene, complete cds.
 ACCESSION M62395
 VERSION M62395.1 GI:173537
 KEYWORDS
 SOURCE
 ORGANISM
 Pichia sp.
 Pichia sp.
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Pichia.
 REFERENCE
 1 (bases 1 to 1048)
 Kawai, S., Murao, S., Mochizuki, M., Yano, K. and Takagi, M.
 Drastic alteration of cycloheximide sensitivity by substitution of
 one amino acid in the L41 ribosomal protein of yeasts
 Unpublished (1992)
 COMMENT
 Original source text: C.maltosa (strain IAM12247) rRNA.
 FEATURES
 source
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 Location/Qualifiers
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 Db 749 TTCCAAAGACCAAGAGAACTTCTGCAAGGTAAGACTGCGTAAGCACACCAACACA 808
 Qy 621 AGGTGACCCAGTACAGAGGAAAGACTCCATCTTCGCCAGGAAAGCGAGTACG 680
 Db 809 AGGTGACCCATACAGAGGTAAGGCTCTTTGTTGCCAGGGTAAGAGATATG 868
 Qy 681 ACCGAAAGCAGTCGGTTACGAGGTACAGCAAGCCGTTTCCACAAGAGCTAAGA 740
 Db 869 ACCGTAAGCAATCGGTTTCGGTGTCAACCAAGCCGTTTCCACAAGAGCCCAAGA 928
 Qy 741 CCACCAAGAGGTGCTCTTCGATTGG 767
 Db 929 CTACCAAGAGGTGTTGTGATTGG 955
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 VERSION AR065319.1 GI:5995535
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 2086)
 Kondo, K., Kajiwara, S. and Misawa, N.
 Transformation systems for the yeast candida utilis and the
 expression of heterologous genes therewith
 Patent: US 5849524-A 5 15-DEC-1998;
 Location/Qualifiers

FEATURES
 source Location/Qualifiers
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 VERSION D10406.1 GI:218112
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 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (sites)
 Uchimiya,H., Kidou,S., Shimazaki,T., Aotsuka,S., Takamatsu,S.,
 Nishi,R., Hashimoto,H., Matsubayashi,Y., Kidou,N., Umeda,M. and
 Kato,A.
 Random sequencing of cDNA libraries reveals a variety of expressed
 genes in cultured cells of rice (Oryza sativa L.)
 Plant J. 2, 1005-1009 (1992)
 2 (bases 1 to 444)
 Kidou,S., Umeda,M., Kato,A. and Uchimiya,H.
 Plant cDNA homologue to rat insulinoma gene encoding ribosomal
 protein S15
 Nucleic Acids Res. 21 (8), 2013 (1993)
 93261842
 8493114
 3 (bases 1 to 444)
 Uchimiya,H.
 Direct Submission
 Submitted (27-JAN-1992) Hirofumi Uchimiya, Institute of Mol. &
 Cell. Bioscience, The University of Tokyo, Department of Cellular
 Function, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan
 (E-mail:huchimi@tansei.cc.u-tokyo.ac.jp)
 Tel:03-3812-2111(ex.7844), Fax:03-3812-2910
 Submitted (27-Jan-1992) to DDBJ by:
 Hirofumi Uchimiya
 Institute of Applied Microbiology

University of Tokyo
 Bunkyo-ku, Tokyo 113
 Japan
 Phone: 03-3812-2111 x7844
 Fax: 03-3812-291
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 110 TTCAAAGGTCACCTCAGTACAGGAGGTAAGGACAGCCTGTCTGCCAGGNAAGCGCC 169
 675 GATACGACCGAAAGCAGTCGCGTTACGAGGTACAGCAAGCCGTTTCCACAAAGAGG 734
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 insert sequence.
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 VERSION AK058924.1 GI:32968942
 KEYWORDS FLI cDNA; oligo-capping.
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Ehrhartoideae; Oryzeae; Oryza.
 1
 The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team,
 Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
 Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
 Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
 Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group, Otomo,Y., Murakami,K.,
 Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
 Kuroaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
 Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
 Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
 Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
 Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
 Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
 Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Otsu,N., Oka,Y.,
 Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
 Yoshino,M. and Hayashizaki,Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice
 Science 301 (5631), 376-379 (2003)
 22752273
 12869764
 2 (bases 1 to 676)
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
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 Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
 Kanagawa,S., Kato,H., Kawagashira,N., Kawai,J., Kawamata,M.,

Yanamoto, M.
 PAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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 Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
 Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
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 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
 Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
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 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P.,
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 Location/Qualifiers
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 /clone="J023009C02"

FEATURES

source

ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 08:40:39 ; Search time 739.931 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	119.8	9.8	467	10	ADK59686 Plant DNA
6	119.4	9.8	495	3	AAF07944 Fusarium
7	112.2	9.2	513	3	AAF11322 Aspergill
8	110.6	9.0	519	10	ADC75158 T harzian
9	110.6	9.0	659	10	ADK56011 Plant DNA
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37	94.2	7.7	491	10	ADC75159	Adc75159 T harzian
38	94.2	7.7	536	12	ADJ42888	Adj42888 Plant cDN
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c 45	93.2	7.6	443	6	ABL94083	Ab194083 Arabidops

ALIGNMENTS

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DT 15-SEP-2003 (revised)
DT 25-SEP-2000 (first entry)
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XX
KW Astaranthin; L41; yeast; carotenoid; cyclohexamide-resistance;
KW site-directed mutagenesis; selectable marker; ribosomal DNA; da.
XX Xanthophyllomyces dendrorhous.
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 XX PD 11-MAY-2000.
 XX PF 29-MAY-1999; 99WO-KR000265.
 XX PR 31-OCT-1998; 98KR-00046547.
 XX XX {KOAD } KOREA ADV INST SCI & TECHNOLOGY.
 XX PA (HAIT-) HAI TAI CONFECTIONERY CO LTD.
 XX XX

PI Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;
 PI Choi SK, Son YR;
 XX WPI; 2000-365630/31.
 DR P-PSDB; AAY94261.
 XX
 XX Novel vector comprising a cyclohexamide-resistance gene and a ribosomal
 FT DNA useful for the transformation of Phaffia rhodozyma.
 XX PS Disclosure; Fig 1; 43pp; English.
 XX
 CC The present genomic sequence is the L41 gene encoding a Phaffia rhodozyma
 CC ribosomal protein. The present sequence is the wild-type sequence, with a
 CC proline residue at position 56. This residue is responsible for P.
 CC rhodozyma sensitivity to cyclohexamide. However, when this residue is
 CC mutated via site-directed mutagenesis to give rise to a glutamine at
 CC position 56, the yeast gains resistance to cyclohexamide. The modified
 CC L41 gene can be used as a selectable marker of a transforming vector for
 CC P. rhodozyma. The vector can be used to carry foreign DNA, e.g. the
 CC astaxanthin gene, a carotenoid. A Phaffia rhodozyma rDNA gene can also be
 CC included in the vector to enhance the integration efficiency of foreign
 CC DNA into host genomes. (Updated on 15-SEP-2003 to standardise OS field)
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QY 1081 CCTTTTGGTTCGAGTGTCTTCTATFCGGTGTGTCTTCTTCTTCTTGATGATATC 1140
Db 1785 CCTTTTGGTTCGAGTGTCTTCTATFCGGTGTGTCTTCTTCTTCTTGATGATATC 1844
QY 1141 ATTTATCGTGTGACGTGTTTCTCTGCTGCTGTTCTCTCTCTCTGTTGCTTCT 1200
Db 1845 ATTTATCGTGTGACGTGTTTCTCTGCTGCTGTTCTCTCTCTCTGTTGCTTCT 1904
QY 1201 CAGGAGCGGCATCTCTTTCTAA 1223
Db 1905 CAGGAGCGGCATCTCTTTCTAA 1927

RESULT 3
AA15568
ID AA15568 standard; cdna; 347 BP.
XX AC AA15568;
XX AC
XX AC
DT 15-SEP-2003 (revised)
DT 25-SEP-2000 (first entry)
XX Phaffia rhodozyma L41 cdna.
XX DE
XX DE
XX KW Astaxanthin; L41; yeast; carotenoid; cyclohexamide-resistance;
XX KW site-directed mutagenesis; selectable marker; ribosomal DNA; ss.
XX OS Xanthophyllomyces dendrorhous.
XX FH Key Location/Qualifiers
XX CDS 30..350
XX FT /*tag= a
XX FT /product= "L41 protein"
XX
XX FN WO200026387-A1.
XX
XX PD 11-MAY-2000.
XX PD
XX PF 29-MAY-1999; 99WO-KR000265.
XX PF
XX PR 31-OCT-1998; 98KR-00046547.
XX PR
XX PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX PA (HAIT-) HAI TAI CONFECTIONERY CO LTD.

PI Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;
PI Choi SK, Son YR;
XX WPI; 2000-365630/31.
DR P-PSDB; AAY94261.
XX
XX Novel vector comprising a cyclohexamide-resistance gene and a ribosomal
PT DNA useful for the transformation of Phaffia rhodozyma.
XX
XX Claim 3; Page 36-37; 43pp; English.
XX
XX The present cDNA sequence is the L41 gene encoding a Phaffia rhodozyma
CC ribosomal protein. The present sequence is the wild-type sequence, with a
CC proline residue at position 56. This residue is responsible for P.
CC rhodozyma sensitivity to cyclohexamide. However, when this residue is
CC mutated via site-directed mutagenesis to give rise to a glutamine at
CC position 56, the yeast gains resistance to cyclohexamide. The modified
CC L41 gene can be used as a selectable marker of a transforming vector for
CC P. rhodozyma. The vector can be used to carry foreign DNA, e.g. the
CC astaxanthin gene, a carotenoid. A Phaffia rhodozyma rDNA gene can also be
CC included in the vector to enhance the integration efficiency of foreign
CC DNA into host genomes. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 347 BP; 103 A; 98 C; 87 G; 59 T; 0 U; 0 Other;
SQ
Query Match 12.1%; Score 147.6; DB 3; Length 347;
Best Local Similarity 97.4%; Pred. No. 6.7e-32;
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 616 TCTGTAGTGTGACCCAGTACAGAGGAAAGGAGTCCATCTTCGCCAGGAAAGCGACG 675
Db 95 TCACAAAGGTGACCCAGTACAGAGGAAAGGAGTCCATCTTCGCCAGGAAAGCGACG 154
QY 676 ATACGACCGAAAGAGTCCGGTTACGAGGTTCAGACCAAGCCCGTTTCCACAAAGAGC 735
Db 155 ATACGACCGAAAGAGTCCGGTTACGAGGTTCAGACCAAGCCCGTTTCCACAAAGAGC 214
QY 736 TAAGACCAACCAAGAGTTCCTTCGATTGGCG 769
Db 215 TAAGACCAACCAAGAGTTCCTTCGATTGGAG 248
RESULT 4
ADC76428
ID ADC76428 standard; DNA; 467 BP.
XX AC ADC76428;
XX AC
XX AC
DT 01-JAN-2004 (first entry)
XX
XX DE DNA homologous to phytopathogen resistance-related cdna - SEQ ID 1697.
XX DE rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX KW phytopathogen; gene shuffling; ds.
XX OS Unidentified.
XX
XX PN WO2003020905-A2.
XX PD 13-MAR-2003.
XX PF 30-AUG-2002; 2002WO-US027883.
XX PF 31-AUG-2001; 2001US-0316392P.
XX PR (DOWC) DOW CHEM CO.
XX PA Shukla V, Butler H, Larrinua I, Reddy AS;
XX PI WPI; 2003-290185/28.
XX DR
XX PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver

PT rheas, useful for conferring disease resistance in plants.
 XX
 PS Claim 1; SEQ ID NO 1697; 617pp; English.
 CC
 CC The invention relates to a novel isolated nucleic acid derived from
 CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
 CC (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas
 CC (poppy) and a sequence that hybridises to them under conditions of low
 CC stringency, where expression of the nucleic acid in a plant results in a
 CC disease resistance phenotype. The polynucleotides of the invention
 CC demonstrate anti-fungal activity and may be useful in conferring disease
 CC resistance in a plant against phytopathogen such as Aspergillus flavus,
 CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
 CC polynucleotides may be useful to retrieve unknown sequences and in gene
 CC shuffling or sexual PCR procedures. The current sequence is that of the
 CC DNA of the invention which is homologous to that of the phytopathogen
 CC resistance-related contig cDNAs.
 XX
 SQ Sequence 467 BP; 119 A; 134 C; 126 G; 88 T; 0 U; 0 Other;
 Query Match 9.8%; Score 119.8; DB 10; Length 467;
 Best Local Similarity 88.4%; Pred. No. 7.7e-24;
 Matches 130; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 621 AGGTGACCCAGTACAGAGGGAAGGAGTCCATCTTCGCCAGGGAAGGAGGATACG 680
 DB 107 AGGTGACCCAGTACAGAGGCTGGCAAGGCTCCCTCTTCGCCAGGGAAGGCTGTTACG 166
 QY 681 ACCGAAGAGCGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 740
 DB 167 ACCGTAAGCAGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 226
 QY 741 CCACCAAGAAGGTCGTCCTTCGATTGG 767
 DB 227 CCACCAAGAAGGTCGTCCTTCAGATTAG 253
 RESULT 5
 ADKS9686
 ID. ADKS9686 standard; DNA; 467 BP.
 XX
 AC ADKS9686;
 XX
 DT 06-MAY-2004 (first entry)
 DE
 XX Plant DNA sequence which confers altered metabolic characteristic #7069.
 XX altered metabolic characteristic; plant; acid metabolism;
 KW alcohol metabolism; fatty acid metabolism;
 KW branched fatty acid metabolism; alkaloid metabolism;
 KW amino acid metabolism; ester metabolism; glyceride metabolism;
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
 XX
 OS Unidentified.
 XX
 XX WO2003020936-A1.
 XX
 PD 13-MAR-2003.
 XX
 XX 30-AUG-2002; 2002WO-US027884.
 XX
 XX 31-AUG-2001; 2001US-0316471P.
 XX
 XX (DOWC) DOW CHEM CO.
 XX (DOWC) DOW AGROSCIENCES LLC.
 XX
 XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
 XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
 XX WPI; 2003-313091/30.
 DR

XX Novel genes that confer altered metabolic characteristics in Nicotiana
 PT benthamiana plants, useful for altering the levels of metabolites e.g.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
 XX
 PS Claim 1; SEQ ID NO 7069; 2576pp; English.
 CC
 CC The invention comprises DNA sequences which confer an altered metabolic
 CC characteristic when they are expressed in a plant. The DNA sequences of
 CC the invention are useful for producing plants with an altered metabolic
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,
 CC altered glyceride metabolism, altered phenolic metabolism, altered
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.
 XX
 SQ Sequence 467 BP; 119 A; 134 C; 126 G; 88 T; 0 U; 0 Other;
 Query Match 9.8%; Score 119.8; DB 10; Length 467;
 Best Local Similarity 88.4%; Pred. No. 7.7e-24;
 Matches 130; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 621 AGGTGACCCAGTACAGAGGGAAGGAGTCCATCTTCGCCAGGGAAGGAGGATACG 680
 DB 107 AGGTGACCCAGTACAGAGGCTGGCAAGGCTCCCTCTTCGCCAGGGAAGGCTGTTACG 166
 QY 681 ACCGAAGAGCGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 740
 DB 167 ACCGTAAGCAGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 226
 QY 741 CCACCAAGAAGGTCGTCCTTCGATTGG 767
 DB 227 CCACCAAGAAGGTCGTCCTTCAGATTAG 253
 RESULT 6
 AAF07944
 ID. AAF07944 standard; cDNA; 495 BP.
 XX
 AC AAF07944;
 XX
 DT 13-MAR-2001 (first entry)
 DE
 XX Fusarium venenatum EST SEQ ID NO:467.
 XX
 DE Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Fusarium venenatum.
 XX
 XX WO200056762-A2.
 XX
 XX 28-SEP-2000.
 XX
 XX 22-MAR-2000; 2000WO-US007781.
 XX
 XX 22-MAR-1999; 99US-00273623.
 XX
 XX (NOVO) NOVO NORDISK BIOTECH INC.
 XX (NOVO) NOVO NORDISK AS.
 XX
 XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX WPI; 2000-594572/56.
 XX

PT Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags.

XX Claim 86; Page 564; 3161pp; English.

XX The present invention describes a method for monitoring differential
XX expression of genes in a first filamentous fungal (FF) cell relative to
XX expression of the same genes in one or more second filamentous fungal
XX cells. The method uses fluorescence-labeled nucleic acids isolated from
XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX are used in the methods for monitoring differential expression of genes
XX in a first filamentous fungal (FF) cell relative to expression of the
XX same genes in one or more second filamentous fungal cells. Monitoring the
XX global expression of genes from FF cells allows the production potential
XX of the microorganisms to be improved. New genes may be discovered.
XX possible functions of unknown open reading frames can be identified and
XX gene copy number variation and stability can be monitored. The expression
XX of genes can be used to study how FF cells adapt to changes in culture
XX conditions, environmental stress, spore morphogenesis, recombination,
XX metabolic or catabolic pathway engineering. Using ESTs provides several
XX advantages over genomic or random cDNA clones including elimination of
XX redundancy as one spot on an array equals one gene or open reading frame,
XX and organisation of the microarrays based on function of the gene
XX products to facilitate analysis of the results. AAF07478 to AAF11247
XX represents ESTs from *Fusarium venenatum*; AAF11248 to AAF11853 represents
XX ESTs from *Aspergillus niger*; AAF11854 to AAF14878 represents ESTs from
XX *Aspergillus oryzae*; and AAF14879 to AAF15337 represents ESTs from
XX *Trichoderma reesei*, which are all specifically claimed in the present
XX invention

SQ Sequence 495 BP; 132 A; 120 C; 119 G; 107 T; 0 U; 17 Other;

Query Match 9.8%; Score 119.4; DB 3; Length 495;

Best Local Similarity 86.6%; Pred. No. 1e-23; Indels 0; Gaps 0;

Matches 129; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGAGGAGCGATACG 680

DB 80 AGGTCAACCACTACAAAGGCTGGAAGGCTCCCTGTCGCCAGGAGGCTCNATATG 139

QY 681 ACCGAAACGATCCGGTTACGAGGTTCAGACCAAGCCGTTTTCACAAAGGCTAAGA 740

DB 140 ACCGCAANCACTCCGGTTATGTTGTCAGACCAANCCGTTCTCCCAANAAGGCCAAGA 199

QY 741 CCACCAAGAAGTCTGCTTCGATTGGCG 769

DB 200 CCACCAAGAAGTCTGCTTCGATTGGAG 228

RESULT 7

AAFL1322

ID AAF11322 standard; cDNA; 513 BP.

AC AAF11322;

DT 13-MAR-2001 (first entry)

DE *Aspergillus niger* EST SEQ ID NO:3845.

XX Multiple gene expression; filamentous fungal cell; EST;

KW expressed sequence tag; *Fusarium venenatum*; *Aspergillus niger*;

KW *Aspergillus oryzae*; *Trichoderma reesei*; identification; recombination;

KW culture condition; environmental stress; spore morphogenesis;

KW metabolic pathway engineering; catabolic pathway engineering; ss.

OS *Aspergillus niger*.

XX WO200056762-A2.

PN 28-SEP-2000.

PD 22-MAR-2000; 2000WO-US007781.

XX

XX 22-MAR-1999; 99US-00273623.

PR (NOVO) NOVO NORDISK BIOTECH INC.

PA (NOVO) NOVO NORDISK AS.

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

XX WPI; 2000-594572/56.

XX Monitoring differential expression of genes in filamentous fungal cells

PT uses fluorescence-labeled nucleic acids isolated from the cells and a

PT substrate of expressed sequence tags.

XX Claim 87; Page 1720; 3161pp; English.

XX The present invention describes a method for monitoring differential

CC expression of genes in a first filamentous fungal (FF) cell relative to

CC expression of the same genes in one or more second filamentous fungal

CC cells. The method uses fluorescence-labeled nucleic acids isolated from

CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs

CC are used in the methods for monitoring differential expression of genes

CC in a first filamentous fungal (FF) cell relative to expression of the

CC same genes in one or more second filamentous fungal cells. Monitoring the

CC global expression of genes from FF cells allows the production potential

CC of the microorganisms to be improved. New genes may be discovered.

CC possible functions of unknown open reading frames can be identified and

CC gene copy number variation and stability can be monitored. The expression

CC of genes can be used to study how FF cells adapt to changes in culture

CC conditions, environmental stress, spore morphogenesis, recombination,

CC metabolic or catabolic pathway engineering. Using ESTs provides several

CC advantages over genomic or random cDNA clones including elimination of

CC redundancy as one spot on an array equals one gene or open reading frame,

CC and organisation of the microarrays based on function of the gene

CC products to facilitate analysis of the results. AAF07478 to AAF11247

CC represents ESTs from *Fusarium venenatum*; AAF11248 to AAF11853 represents

CC ESTs from *Aspergillus niger*; AAF11854 to AAF14878 represents ESTs from

CC *Aspergillus oryzae*; and AAF14879 to AAF15337 represents ESTs from

CC *Trichoderma reesei*, which are all specifically claimed in the present

CC invention

XX Sequence 513 BP; 141 A; 128 C; 133 G; 110 T; 0 U; 1 Other;

Query Match 9.2%; Score 112.2; DB 3; Length 513;

Best Local Similarity 84.6%; Pred. No. 1.2e-21;

Matches 126; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGAGGAGCGATACG 680

DB 98 AGGTCAACCACTACAAAGGCTGGAAGGCTCCCTGTCGCCAGGAGGCTCGTTACG 157

QY 681 ACCGAAACGATCCGGTTACGAGGTTCAGACCAAGCCGTTTTCACAAAGGCTAAGA 740

DB 158 ACCGGAAGCAGAGCGGTTATGTTGTCAGACCAAGCCGTTCTCCCAAGAAGGCCAAGA 217

QY 741 CCACCAAGAAGTCTGCTTCGATTGGCG 769

DB 218 CCACCAAGAAGTCTGCTTCGTTTGAG 246

RESULT 8

ADC75158

ID ADC75158 standard; cDNA; 519 BP.

XX ADC75158;

DT 01-JAN-2004 (first entry)

XX T harzianum phytopathogen resistance-related contig cDNA - SEQ ID 82.

DE rice; yeast; poppy; plant; disease resistance; anti-fungal;

XX phytopathogen; gene shuffling; ss.

KW

XX

Unidentified.
WO2003020936-A1.
13-MAR-2003.
30-AUG-2002; 2002WO-US027884.
31-AUG-2001; 2001US-0316471P.
(DOWC) DOW CHEM CO.
(DOWC) DOW AGROSCIENCES LLC.
Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Fell RJ;
Oriado JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
WPI; 2003-313091/30.

Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

Claim 1; SEQ ID NO 3394; 2576pp; English.

The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered amino acid metabolism, altered ester metabolism, altered glyceride metabolism, altered phenolic metabolism, altered carbohydrate metabolism, altered sterol, oxygenated terpene, or isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a DNA sequence of the invention.

Sequence 659 BP; 174 A; 160 C; 177 G; 148 T; 0 U; 0 Other;

Query Match 9.0%; Score 110.6; DB 10; Length 659;
Best Local Similarity 83.9%; Pred. No. 4e-21;
Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0

QY 621 AGGTGACCCAGTACAAGAAGGGAAAGACTTCATCTTGCCCCAGGGAAGCGCATACG 680
Db 98 AGGTCACTCAGTACAAGGCCGCATGGTTCTTCCCTGTTCCCGGTAAGACGCTTATG 157

QY 681 ACCGAAGCAGTCCCGTTACGGAGGTTCAGACCAAGCCGTTTTCCACAAGAGGCTAAGA 740
Db 158 ACCGAAGCAGAGCGGTTATGGTGGTCAGACCAAGCCGTTCTTCCACAAGAGGCCAAGA 217

QY 741 CCACCAGAAGGTCTGCTTCGATTGGCG 769
Db 218 CCACCAAGAAGGTCTGCTTCGATTGGAG 246

RESULT 10
ADK56011
ID ADK56011 standard; DNA; 659 BP.
XX AC ADK56011;
XX DT 01-JAN-2004 (first entry)
XX DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 734.
XX KW rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX KW phytopathogen; gene shuffling; ds.
XX OS Unidentified.
XX PN WO2003020905-A2.

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XX PD 13-MAR-2003.
XX PF 30-AUG-2002; 2002WO-US027883.
XX PR 31-AUG-2001; 2001US-0316392P.
XX PA (DOWC ) DOW CHEM CO.
XX PI Shukla V, Butler H, Larrinua I, Reddy AS;
XX DR WPI; 2003-290185/28.
XX PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
XX PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
XX PT rhoeas, useful for conferring disease resistance in plants.
XX PS Claim 1; SEQ ID NO 734; 617pp; English.
XX CC The invention relates to a novel isolated nucleic acid derived from
XX CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
XX CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas
XX CC (poppy) and a sequence that hybridises to them under conditions of low
XX CC stringency, where expression of the nucleic acid in a plant results in a
XX CC disease resistance phenotype. The polynucleotides of the invention
XX CC demonstrate anti-fungal activity and may be useful in conferring disease
XX CC resistance in a plant against phytopathogen such as Aspergillus flavus,
XX CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
XX CC polynucleotides may be useful to retrieve unknown sequences and in gene
XX CC shuffling or sexual PCR procedures. The current sequence is that of the
XX CC DNA of the invention which is homologous to that of the phytopathogen
XX CC resistance-related contig cDNAs.
XX SQ Sequence 669 BP; 180 A; 163 C; 177 G; 149 T; 0 U; 0 Other;

Query Match 9.0%; Score 110.6; DB 10; Length 669;
Best Local Similarity 83.9%; Pred. No. 4e-21;
Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAGAGGGAAGGACTCCATCTGCGCCAGGGAAGCGAGATACG 680
DB 108 AGGTCACTCAGTACAGAGGCGCGGAGGTTTCCCTGTTGCGCCAGGTAAGAGCGTTATG 167
QY 681 ACCGAAAGCAGTCCGGTTACGGAGGTACAGACCAAGCCCGTTTCCACAAAGAGGCTAAGA 740
DB 168 ACCGGAAGCAGAGCGGTTATGTTGTGTGTCAGACCAAGCCCGTCTTCCACAAAGGCCCAAGA 227
QY 741 CCACCAAGAGGTGCTCTTCGATTGGCG 769
DB 228 CCACCAAGAGGTGCTCTCGCGTTGGAG 256

RESULT 11
ADK59682
ID ADK59682 standard; DNA; 669 BP.
XX AC ADK59682;
XX DT 06-MAY-2004 (first entry)
XX DE Plant DNA sequence which confers altered metabolic characteristic #7065.
XX KW altered metabolic characteristic; plant; acid metabolism;
XX KW alcohol metabolism; fatty acid metabolism;
XX KW branched fatty acid metabolism; alkaloid metabolism;
XX KW amino acid metabolism; ester metabolism; glyceride metabolism;
XX KW phenolic metabolism; carbohydrate metabolism; steroid metabolism;
XX KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
XX KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
XX KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX OS Unidentified.

PN WO2003020936-A1.
XX PD 13-MAR-2003.
XX PF 30-AUG-2002; 2002WO-US027884.
XX PR 31-AUG-2001; 2001US-0316471P.
XX PA (DOWC ) DOW CHEM CO.
XX PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX DR Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX PT WPI; 2003-313091/30.
XX PT Novel genes that confer altered metabolic characteristics in Nicotiana
XX PT benthamiana plants, useful for altering the levels of metabolites e.g.
XX PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX PS Claim 1; SEQ ID NO 7065; 2576pp; English.
XX CC The invention comprises DNA sequences which confer an altered metabolic
XX CC characteristic when they are expressed in a plant. The DNA sequences of
XX CC the invention are useful for producing plants with an altered metabolic
XX CC characteristic, such as: altered acid metabolism, alcohol metabolism,
XX CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX CC base metabolism, altered amino acid metabolism, altered ester metabolism,
XX CC altered glyceride metabolism, altered phenolic metabolism, altered
XX CC carbohydrate metabolism, altered steroid, oxygenated terpene, or
XX CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX CC metabolism, ketone or quinone metabolism. The DNA sequences of the
XX CC invention may be used to provide disease resistance in a plant and gene
XX CC shuffling or sexual PCR procedures. The present nucleic acid represents a
XX CC DNA sequence of the invention.
XX SQ Sequence 669 BP; 180 A; 163 C; 177 G; 149 T; 0 U; 0 Other;

Query Match 9.0%; Score 110.6; DB 10; Length 669;
Best Local Similarity 83.9%; Pred. No. 4e-21;
Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAGAGGGAAGGACTCCATCTGCGCCAGGGAAGCGAGATACG 680
DB 108 AGGTCACTCAGTACAGAGGCGCGGAGGTTTCCCTGTTGCGCCAGGTAAGAGCGTTATG 167
QY 681 ACCGAAAGCAGTCCGGTTACGGAGGTACAGACCAAGCCCGTTTCCACAAAGAGGCTAAGA 740
DB 168 ACCGGAAGCAGAGCGGTTATGTTGTGTGTCAGACCAAGCCCGTCTTCCACAAAGGCCCAAGA 227
QY 741 CCACCAAGAGGTGCTCTTCGATTGGCG 769
DB 228 CCACCAAGAGGTGCTCTCGCGTTGGAG 256

RESULT 12
AAT08602
ID AAT08602 standard; DNA; 2086 BP.
XX AC AAT08602;
XX DT 16-OCT-2003 (revised)
XX DT 03-DEC-1996 (first entry)
XX DE Ribosomal protein L41 gene.
XX KW Ribosomal protein; expression vector; heterogene; yeast; GAP; PGK; PMA;
XX KW phosphoglyceric acid kinase; protoplasmic membrane proton ATPase;
XX KW glyceraldehyde-3-phosphoric acid dehydrogenase; resistance marker;
XX KW hygromycin B phosphotransferase; aminoglycoside-3'-phosphotransferase;
XX KW ss.
XX OS Pichia jadinii.

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XX FH Key Location/Qualifiers
XX exon 1111..1114
XX FT /*tag= a
XX FT /label= Exon 1.
XX FT intron 1115..1481
XX FT /*tag= b
XX FT /label= Intron 1.
XX FT 1482..1795
XX FT /*tag= c
XX FT /label= Exon 2.
XX FT
XX PN W09532289-A1.
XX
XX PD 30-NOV-1995.
XX
XX PP 25-MAY-1995; 95WO-JP001005.
XX
XX PR 25-MAY-1994; 94JP-00135015.
XX PR 26-OCT-1994; 94JP-00285823.
XX PR 28-APR-1995; 95JP-00129287.
XX
XX PA (KIRI ) KIRIN BEER KK.
XX
XX PI Kondo K, Kajiwara S, Misawa N;
XX WPI; 1996-020584/02.
XX
XX DR Ribosomal protein L41 gene, promoter and terminator sequences, isolated
XX PT from Candida utilis - used in vector for expression of hetero:gene(s) in
XX PT yeast.
XX
XX PS Claim 4; Page 159-161; 252pp; Japanese.
XX
XX CC The L41 ribosomal structural protein gene can be used in the construction
XX CC of expression vectors designed specifically to express heterogenes in
XX CC yeast. The vectors also comprise: a promoter and terminator sequence
XX CC selected from phosphoglyceric acid kinase (PGK), glyceraldehyde-3-
XX CC phosphoric acid dehydrogenase (GAP) and protoplasmic membrane proton
XX CC ATPase (PMA) genes isolated from Candida utilis; a drug resistance marker
XX CC selected from aminoglycoside-3'-phosphotransferase or hygromycin B
XX CC phosphotransferase; and the heterogene to be expressed. L41 confers
XX CC cyclohexamine resistance on the yeast. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 2086 BP; 591 A; 458 C; 529 G; 508 T; 0 U; 0 Other;

Query Match 8.8%; Score 107.8; DB 2; Length 2086;
Best Local Similarity 79.9%; Pred. No. 4.2e-20;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680
DB 1548 AGGTATCCAGTACAAAGGCTGGTAAGGCTTCCTCTTTGCCAGGTAAGCGTGTATG 1607

QY 681 ACCGAAAGCAGTCCGGTTACGGAGTTCAGACCAAGCCCGTTTCCACAAGAGCTAAGA 740
DB 1608 ACCGTAGCAATCCGTTACGGTGTCTCAACCAAGCCAGTTTCCACAAAAGGCTAATA 1667

QY 741 CCACCAAGAGGTCGTCCTTCGATTCGGCGGTATTTTGT 779
DB 1668 CCACCAAGAGGTTGTTTTCGTTTGGAGTGTGTGTCT 1706

RESULT 13
AAV31513
ID AAV31513 standard; DNA; 2086 BP.
XX
XX AC AAV31513;
XX
XX DT 17-OCT-2003 (revised)
XX DT 14-AUG-1998 (first entry)
XX

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DE Base sequence of DNA fragment containing L41 gene.
XX
XX KW Candida utilis; yeast vector; promoter; marker gene; GAP gene;
XX KW high-efficiency integration; monellin; food; drug; L41; URA3; ss.
XX
XX OS Pichia jadinii.
XX
XX FH Key Location/Qualifiers
XX CDS 1111..1798
XX FT /*tag= a
XX FT /note= "contains intron"
XX FT intron 1117..1482
XX FT /*tag= b
XX FT /number= 1
XX FT /cons_splice= (5'site=Yes, 3'site=No)
XX
XX PN W09807873-A1.
XX
XX PD 26-FEB-1998.
XX
XX PP 22-AUG-1997; 97WO-JP002924.
XX
XX PR 23-AUG-1996; 96JP-00241062.
XX
XX PA (KIRI ) KIRIN BEER KK.
XX
XX PI Kondo K, Miura Y;
XX
XX DR WPI; 1998-169177/15.
XX DR P-PSDB; AAW57490.
XX
XX PT Yeast vector for multi-copying on to chromosomes of yeast such as Candida
XX PT utilis - contains a shortened promoter sequence linked to a marker gene
XX PT for high-efficiency integration.
XX
XX PS Example; Fig 9; 107pp; Japanese.
XX
XX CC This represents the base sequence of DNA fragment containing yeast L41
XX CC gene. This can be used in the construction of a yeast vector for multi-
XX CC copying on to chromosomes of yeast such as Candida utilis. The vector
XX CC contains a DNA homologous with a chromosomal gene of the yeast
XX CC (preferably ribosomal DNA (rDNA) such as the URA3, L41, PGK, GAP or PMA
XX CC gene), a marker gene to be used in transformant selection (such as a drug
XX CC resistance gene, e.g. the cycloheximide resistance gene L41, the G418
XX CC resistance gene Tn903-APT, or the hygromycin B resistance gene (from
XX CC E.coli) HPT), a shortened promoter sequence such as the C.utilis L41,
XX CC phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dihydrogenase
XX CC (GAP) or plasma membrane proton ATPase (PMA) gene promoter and a gene of
XX CC interest from yeast or other origin. The vectors are useful in the
XX CC preparation of proteins for food or drug use in high efficiency. They can
XX CC be used especially for the production of single-chain monellin, which is
XX CC a low-calorie sweetener whose thermostability is greater than that of the
XX CC dimeric natural monellin. Multiple copies of the desired gene are
XX CC integrated into the yeast chromosome and high expression efficiency is
XX CC obtained. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 2086 BP; 591 A; 458 C; 529 G; 508 T; 0 U; 0 Other;

Query Match 8.8%; Score 107.8; DB 2; Length 2086;
Best Local Similarity 79.9%; Pred. No. 4.2e-20;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680
DB 1548 AGGTATCCAGTACAAAGGCTGGTAAGGCTTCCTCTTTGCCAGGTAAGCGTGTATG 1607

QY 681 ACCGAAAGCAGTCCGGTTACGGAGTTCAGACCAAGCCCGTTTCCACAAGAGCTAAGA 740
DB 1608 ACCGTAGCAATCCGTTACGGTGTCTCAACCAAGCCAGTTTCCACAAAAGGCTAATA 1667

QY 741 CCACCAAGAGGTCGTCCTTCGATTCGGCGGTATTTTGT 779
DB 1668 CCACCAAGAGGTTGTTTTCGTTTGGAGTGTGTGTCT 1706

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RESULT 14
ADJ43725
ID ADJ43725 standard; cdna; 318 BP.
XX AC ADJ43725;
XX DT 06-MAY-2004 (first entry)
XX DE Plant cdna #4725.
XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX OS Eukaryota.
XX PN US2004016025-A1.
XX PD 22-JAN-2004.
XX PF 26-SEP-2002; 2002US-00260238.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.
XX PA (BUDW/) BUDWORTH P.
XX PA (MOUG/) MOUGHAMER T.
XX PA (BRIG/) BRIGGS S P.
XX PA (COOP/) COOPER B.
XX PA (GLAZ/) GLAZEBROOK J.
XX PA (GOFF/) GOFF S A.
XX PA (KATA/) KATAGIRI F.
XX PA (KREP/) KREPS J.
XX PA (PROV/) PROVART N.
XX PA (RICK/) RICHE D.
XX PA (ZHUT/) ZHU T.
XX PI Budworth P, Moughamer T, Briggs SP, Provart N, Ricke D, Zhu T;
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX DR WPT; 2004-190374/18.
XX PS New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Example 13; SEQ ID NO 4725; 230pp; English.
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX CC encode are useful for manipulating crop plants to alter or improve
XX CC phenotypic characteristics, to produce large quantities of oil or
XX CC proteins, to incur resistance to insecticides, viruses or fungi, and to
XX CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX CC have a high nutritional value with reduced apical dominance or dwarfism,
XX CC early flowering or altered metabolic pathways. This sequence represents a
XX CC plant nucleic acid of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification but was obtained in
XX CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

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XX SQ Sequence 318 BP; 103 A; 77 C; 83 G; 55 T; 0 U; 0 Other;
Query Match 8.5%; Score 104.2; DB 12; Length 318;
Best Local Similarity 81.2%; Pred. No. 2e-19;
Matches 121; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Oy 611 CTGTTTCTGTAGTGACCCAGTACAGAGGAGGAAAGGACTCCATCTTTCGCCCGGAAAG 670
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 CTCCTTCACAGGTCACCTCAGTACAGAGGTAAGGACAGCCTGTCTGCCAGGAAAG 123
Oy 671 CGACGATACGACCGAAAGCGAGTCGCTTACGGAGTCAGACCAAGCCCGTTTCCACAAG 730
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 CGCGTTTATGACCGTAAGCAGTCAGGATATCGTGTGAGCAGGAGCTGTCTTCCACAAG 183
Oy 731 AAGGCTAAGACCCCAAGAGGTCGCT 759
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 AAGGCAAAACCCACCAAGAGATTGTGCT 212
RESULT 15
ADJ43721
ID ADJ43721 standard; cdna; 315 BP.
XX AC ADJ43721;
XX DT 06-MAY-2004 (first entry)
XX DE Plant cdna #4721.
XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX OS Eukaryota.
XX PN US2004016025-A1.
XX PD 22-JAN-2004.
XX PF 26-SEP-2002; 2002US-00260238.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.
XX PA (BUDW/) BUDWORTH P.
XX PA (MOUG/) MOUGHAMER T.
XX PA (BRIG/) BRIGGS S P.
XX PA (COOP/) COOPER B.
XX PA (GLAZ/) GLAZEBROOK J.
XX PA (GOFF/) GOFF S A.
XX PA (KATA/) KATAGIRI F.
XX PA (KREP/) KREPS J.
XX PA (PROV/) PROVART N.
XX PA (RICK/) RICHE D.
XX PA (ZHUT/) ZHU T.
XX PI Budworth P, Moughamer T, Briggs SP, Provart N, Ricke D, Zhu T;
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX DR WPT; 2004-190374/18.
XX PS New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Example 13; SEQ ID NO 4721; 230pp; English.

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The invention relates to plant nucleotide sequences that direct seed-, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 315 BP; 103 A; 77 C; 81 G; 54 T; 0 U; 0 Other;

Query Match	8.5%;	Score 103.4;	DB 12;	Length 315;
Best Local Similarity	82.1%;	Pred. No. 3.4e-19;		
Matches 119;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
QY	615	TTCTGTAGGTGACCCAGTACACAAGAGGAAGGACTCCATCTTCGCCCCAGGGAAGGCGAC	674	
Db	65	TTCCACAGGTGCTACTCAGTACAAGAAGGGTATAGGACAGCCTGTCTGCCCCAGGGAAGGCGCC	124	
QY	675	GATACGACCCGAAAGCAGTCCCGGTTTACCGAGGTACAGACCAAGCCCGTTTTTCCACAAGAAGG	734	
Db	125	GTTATGACCGTAGCAGTACAGGATATGTTGGTCAGACCAAGCCTGTTTTTCCACAAGAAGG	184	
QY	735	CTAAGACCAACAAGAGGTGCTCCT	759	
Db	185	CAAAAAACCAACAAGAAGATTGTGT	209	

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